

OM protein - protein search, using sw model

Run on: April 12, 2004, 09:02:37 ; Search time 20 Seconds
(without alignments)
1885.354 Million cell updates/sec

Title: US-09-935-124A-2
Perfect score: 2018
Sequence: 1 MDLFGDLPEPERSRPAAGK.....KAVQGSADNVTVMVVRIGH 392

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	481	23.8	341	2 G86315	hypothetical prote
2	474	23.5	242	2 T18588	probable protein p
3	401.5	19.9	300	2 A5804	phosphoprotein pho
4	370.5	18.4	414	2 S62462	protein phosphatas
5	368	18.2	389	2 T05095	hypothetical prote
6	368	18.2	975	2 T08606	protein phosphatas
7	365	18.1	359	2 T52337	phosphoprotein pho
8	364.5	18.1	348	2 T50783	protein phosphatas
9	362	17.9	464	2 H96700	protein F12A21.5 [
10	358.5	17.8	361	2 T45778	protein phosphatas
11	353.5	17.5	355	2 H84643	probable protein p
12	352.5	17.5	434	2 T04263	phosphoprotein pho
13	352	17.4	392	2 F84650	probable protein p
14	351	17.4	404	2 T00750	probable protein p
15	350	17.3	357	2 T05308	protein phosphatas
16	348	17.2	370	2 S54297	protein phosphatas
17	347	17.2	348	2 E88434	protein T23P1.1 [
18	347	17.2	356	2 T55181	hypothetical prote
19	340	16.8	382	2 S22422	phosphoprotein pho
20	340	16.8	382	2 A32399	phosphoprotein pho
21	338.5	16.8	383	2 T48018	hypothetical prote
22	338.5	16.8	390	2 C84826	protein phosphatas
23	338.5	16.8	405	2 F86206	hypothetical prote
24	338	16.7	382	2 I53823	magnesium dependen
25	337.5	16.7	380	2 E84748	probable protein p
26	336.5	16.7	381	2 T09640	protein phosphatas
27	336.5	16.7	396	2 T02483	probable protein p
28	336	16.7	382	2 S22423	phosphoprotein pho
29	336	16.2	390	2 S65672	phosphoprotein pho

30	326	16.2	393	2 I49016	phosphoprotein pho
31	321.5	15.9	442	2 B86209	protein F22G5.22 [
32	319	15.8	390	2 S20392	phosphoprotein pho
33	319	15.8	397	2 J2524	phosphoprotein pho
34	317.5	15.7	281	2 S41854	phosphoprotein pho
35	309	15.3	468	2 T21331	hypothetical prote
36	307	15.2	816	2 T48123	hypothetical prote
37	306	15.2	347	2 A56058	phosphoprotein pho
38	305.5	15.1	464	2 S8592	hypothetical prote
39	305	15.1	388	2 C85323	protein phosphatas
40	302	15.0	386	2 T09019	phosphoprotein pho
41	300	14.9	491	2 T16354	hypothetical prote
42	297	14.7	423	2 T48121	hypothetical prote
43	292.5	14.5	511	2 F96752	protein phosphatas
44	289	14.3	468	2 S39832	probable phosphopr
45	284	14.1	362	2 F84695	probable protein p

ALIGNMENTS

RESULT 1

G86315
hypothetical protein T10F20.4 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cross)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C/Accession: G86315
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MUID:21016719; PMID:11130712
A/Accession: G86315
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-341 <STO>
A/Cross-references: GB:AE005172; NID:g9719738; PIDN:AAF97840.1; GSPDB:GN00141
C/Genetics:
A/Map position: 1
Query Match 23.8%; Score 481; DB 2; Length 341;
Best Local Similarity 35.8%; Pred. No. 9.2e-28;
Matches 119; Conservative 66; Mismatches 107; Indels 40; Gaps 11;
QY 78 KRKTSEKNGGBELV-----EKKVCKAGSVI-----FGLKGYAERKGEREMQDAHYI 127
DB 24 KAKKSEVSGGGEAVAAVGNRAEDKPSFVSEKKEFLVEADVAEDKGAHTMEDVWV 83
QY 128 LNDITBECPSPSLITRVSYFAVDFGHGGIRASKPAQNLHQNLIKPKGDIVSEKTV 187
DB 84 LPDASLDF--PGTL--RCAHFAIYDGGGRLAAFAKHLHLNLSAGLPRELLDV-KVA 138
QY 188 KRCLLTFKHTDEFLKQASSQKPAWKDSTATCVLAVNLIYIANLGSRAILCR---- 243
DB 139 KKAILEGFRKTDLLIQKSVS--GGWQDGAATVAVCVWILDQKVFANIGAKAVLASST 196
QY 244 -----YNESQKHAALSLSKEHNPTQYERMRKQAGNV-RDGRVLGVLSRSIDGQ 297
DB 197 NELGNHTEAGNPLKATVLTREHKAITYPQERSIKQSGGVSSNGRLQGRLVSRATGDRH 256
QY 298 YKCGVTSPDIRRCOLTPNDRFILLACDGLFKVFTPEEAVNPFILSCLEDEKIQTEGKS 357
DB 257 FKFGVSGATPDIIHAFELTRENFMILGCDLNEVFPSPDAVGFFVQKLL-----KEG-- 307
QY 358 AADARVEAACNRLANKAV-QRGSADNVTVMVV 388
DB 308 ---LHVSTVSRRLVKEAVKERRCKNCTAIVI 336

C;Keywords: phosphoric monoester hydrolase

Query Match 19.9%; Score 401.5; DB 2; Length 300;
Best Local Similarity 33.0%; Pred. No. 5.2e-22;
Matches 102; Conservative 53; Mismatches 105; Indels 49; Gaps 9;
QY 99 KASVIFGLKGYVAERKGEREEMQDAHVILNDITECRPSSLLITRVSVFAVDPGHGGIR 158
D 18 QGKSVIFA-----ASEMGWNTMEDAIIHRHDIQD-----VSFVGVPDGHGGRE 63
QY 159 ASKFAAQNHLQNLII--RKPKGDVIVSEKTVKRCCLDTFKHGTDEEFL-----KQASSQKP 211
D 64 VAQFVEKHFDVDELKKNFK-----EKFEEALAKETFLKMDLLELLTPEGQKELAQYKA 116
QY 212 AWKD-----GSTATCVLAVDNILYIANLGDSRAILCRYNESQKHAALSLSKENNPTQYEE 267
D 117 TDTDESAGCTANVALLIYKNTLVANAGDSRSVLCRNNTNH-----DMSVDHKPDNPEE 170
QY 268 RMRIQAGNVRDGRVGLVLEVSRSIGDQYKRCG-----VTSVPDIRRCQLTPNDR 319
D 171 KSRIERAGGFSVSDGRVNGNLNLSRALCDLEYKFDNKLRSNEQLIIALPDVKYKTELPQDK 230
QY 320 FILLACDGLFKVFTPEAVNFILSCLEDEKIQREKSAADARYEAACNRLANKAVQSGS 379
D 231 FILMGCDGVFETLHQLKQVNSTGGAQVTELLKKAAB-----DLDDQLLAPDTSQGTG 287
QY 380 ADNVTVWVV 388
D 288 CDNMTILV 296

RESULT 4

S62462
Protein phosphatase 2c homolog 3 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 15-Jun-2001
C;Accession: T38573; S54298; S62462
R;Badcock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, October 1995
A;Reference number: Z21745
A;Accession: T38573
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-414 <BA2>
A;Cross-references: EMBL:Z54354; NID:g1019398; PIDN:CAA91172.1; PID:g1019405; GSPDB:GNC
A;Experimental source: strain 972h-; cosmid C2G11
R;Shiozaki, K.; Russell, P.
EMBO J. 14, 492-502, 1995
A;Title: Counteractive roles of protein phosphatase 2C (PP2C) and a MAP kinase kinase
A;Reference number: S54297; MUID:95163582; PMID:7859738
A;Accession: S54298
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-195,'T',197-414 <SHI>
A;Cross-references: EMBL:L34882; NID:g609657; PIDN:AAA67321.1; PID:g609658
C;Genetics:
A;Gene: SPAC2G11.07c
A;Map position: 1L
A;Introns: 110/1; 134/3
C;Superfamily: human phosphoprotein phosphatase 1A

Query Match 18.4%; Score 370.5; DB 2; Length 414;
Best Local Similarity 32.9%; Pred. No. 1.5e-19;
Matches 108; Conservative 53; Mismatches 100; Indels 67; Gaps 13;
QY 81 TSEEEKNGSELVEKVKYKASSVIFGLKGYVAERKGEREEMQDAHVILNDITECRPSS 140
D 10 TEKHSVNGSNEF-----VLYGL-----SSVQGWRIEMDAHSAL--LSMEC---SA 50
QY 141 LITRVSVFAVDPGHGGIRASKFAAQNHLQNLIRK--FPKGDVIVSEKTVKRCCLDT 194
D 51 VKDPVDFFAVVDGGGKVAKWCNSLPQILEKNPDKGDFVNAKLSKSFNADKALD- 109

RESULT 2
T18588
Probable protein phosphatase - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T18588; T21693
R;Mortimore, B.
submitted to the EMBL Data Library, December 1998
A;Reference number: Z18993
A;Accession: T18588
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-242 <WIL>
A;Cross-references: EMBL:AL031264; PIDN:CAA20326.1; GSPDB:GN00020; CBSP:F33A8.6
A;Experimental source: clone VF45E10L
R;Matthews, L.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19459
A;Accession: T21693
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-242 <W12>
A;Cross-references: EMBL:Z81525; PIDN:CAB04260.1; GSPDB:GN00020; CBSP:F33A8.6
A;Experimental source: clone F33A8
C;Genetics:
A;Gene: CBSP:F33A8.6
A;Map position: 2
A;Introns: 28/1; 65/2; 101/1; 133/2; 202/2

Query Match 23.5%; Score 474; DB 2; Length 242;
Best Local Similarity 40.2%; Pred. No. 1.9e-27;
Matches 98; Conservative 54; Mismatches 80; Indels 12; Gaps 5;
QY 82 SBEKNGSBEV-----EKKVKASSVIFGLKGYVAERKGEREEMQDAHVILN--DITEEC 135
D 3 SSKRKSDDLDNSDESKPKESRNLVCTLAAYGCKGERADMDTHIMLPKFDLGTG- 61
QY 136 RPPSSLLITRVSVFAVDPGHGGIRASKFAAQNHLQNLIRKPKK-GDVIVSEKTVKRCCLDT 194
D 62 ---KSFLSRASPPAIFDGHAGPRAAHSQSMGKTVKEKLAKFSDFPILTKSLKQTFTES 118
QY 195 FKHTEDEFLKQASSQKPAKDGSTATCVLAVDNILYIANLGDSRAILCRYNESQKHAAL 254
D 119 YKAVDDGFLAIAKQNKPIWKDGTATTMIILNNVIYVANGDSRAVARKKEDG-SFAPV 177
QY 255 SLKSKHNPTCYERMRIOKAGNVRDGRVGLVLEVSRSIGDQYKRCGVTSPDIRRCQL 314
D 178 CLTVDDHPSHDERMRIQAGAVVKDGRINGVIEVSRSIGDLPFKSLGIISTPDLKLT 237
QY 315 TPND 318
D 238 TKND 241

RESULT 3

A55804
Phosphoprotein phosphatase (EC 3.1.3.16) 2c, membrane-bound - Paramoecium tetraurelia
C;Species: Paramoecium tetraurelia
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 07-Dec-1999
C;Accession: A55804
R;Klumpp, S.; Hanke, C.; Donella-Deana, A.; Beyer, A.; Kellner, R.; Pinna, L.A.; Schultz
J. Biol. Chem. 269, 32774-32780, 1994
A;Title: A membrane-bound protein phosphatase type 2C from Paramoecium tetraurelia. Purif
A;Reference number: A55804; MUID:95105156; PMID:7806499
A;Accession: A55804
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-300 <KIU>
A;Cross-references: GB:Z36985; NID:g537421; PID:e1192609; PID:g2654382
C;Genetics:
A;Genetic code: SGCS

submitted to the EMBL Data Library, August 1997
A:Reference number: Z16454
A:Accession: T08606
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-975 <AUB>
A:Cross-references: EMBL:AF019985; NID:g2425120; PID:g2425121
A:Experimental source: strain AX3
C:Genetics:
A:Gene: spnA

Query Match 18.2%; Score 368; DB 2; Length 975;
Best Local Similarity 29.1%; Pred. No. 7.2e-19;
Matches 118; Conservative 56; Mismatches 152; Indels 80; Gaps 17;

QY 8 PEPERSPPAAGKEAQKGLLFDLPPASSTDSGGPGLLFDLPPASSGSGSLATSIS 67
DB 620 PKPPKPKPI--KEPKKPKV--ESKPKKE-----PKPIKPKESKEPKEP 661

QY 68 QMVKTEGKAKRTS-----EEKNGSEEL-----VEKKVKCASSVIFGLKGYVAERKE 117
DB 662 KEPKKTPKPKKTSKVDGAESKNGADSCGNGVGSKIKLESQ--FG-----SLOGR 713

QY 118 REEMQDAHVILNDITECR---PPSLITRVSYFAVFDGHHGIRASKFAAQNLHQNLI-- 172
DB 714 RKNMEDTHVILNLMGAVTYNGPKDI--PISYAVYDGHGGTSTLTLEPTVHNCVNS 771

QY 173 RKFPKGDVISVEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILVIA 232
DB 772 QSFROD-----YEQAFRDYAEADIVIEKCE-----KSGTGVSAALLVGNKLYTA 818

QY 233 NLGDSRAILCRNEESQKHAALS-----LSKEHNPQYEEERMRIQKAGNVDRDGRVLGV 287
DB 819 NVGDSEIVLARAQPNANPKGPTVEPVLLSYKHLASDDQEKVKVTDLGGMIIFNLFGL 878

QY 288 EYRSRIGDGQYKR-----CGVTSVPDIRCOITPNDRIILLACDGLFKVFTPEEAVNFI 342
DB 879 AVSRSGDKKEYKEGKKFC--VSDPVQITWTDLTARDHFFILACDGLWQKVEYDEAVQFV 935

QY 343 SCLEDEKIQTRGKSAADARYEAACNLANKAVQSGADNVTVMVV 388
DB 936 -----QRNIKLGKATE-----ISELLAQSDYDRSGDNITVIVV 970

RESULT 7
T52337
phosphoprotein phosphatase (EC 3.1.3.16) 2C [imported] - common ice plant
C:Species: Mesembryanthemum crystallinum [common ice plant]
C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 01-Mar-2002
C:Accession: T52337
R:Miyazaki, S.; Koga, R.; Bohner, H.J.; Fukuhara, T.
Mol. Gen. Genet. 261, 307-316, 1999
A:Title: Tissue- and environmental response-specific expression of 10 PP2C transcripts
A:Reference number: Z26045; MUID:99200489; PMID:10102366
A:Accession: T52337
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-359 <MIY>
A:Cross-references: EMBL:AF075580; PIDN:AAC36698.1
C:Genetics:
A:Gene: PP2C
C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.220
C:Keywords: phosphoric monoester hydrolase

Query Match 18.1%; Score 365; DB 2; Length 359;
Best Local Similarity 31.8%; Pred. No. 3.1e-19;
Matches 92; Conservative 59; Mismatches 94; Indels 44; Gaps 10;

QY 116 GREEEMQDAFVILNDITEE-----CRPPSSLITRVSYFAVFDGHHGIRASKFAAQNLHQ 169
DB 58 GPKYMEDEHIRDDLSVQLGSLFRCPKPS-----AFYGVFDGHHGSEAAAYVRENVMR 111

QY 170 NLIR--KFPKG-----DVISVEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKDGTATCVLA 224

195 FKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDRAILCRNEESQKHAAL 254
DB 110 ----DDQFHTDPS-----GCTATVLRVGNKLYCANAGDSRTVL-----GSKGIK 151

QY 255 SLSEKHNPTQYEEERMRIQKAGNVDRDGRVLGVLEVSRSIGDGQYKRCG-----VTSVP 307
DB 152 PLSADHKPESNAEKARICAGGFDVGRVGNLALSRAIGDFEFKNSNLEPEKQIVTALP 211

QY 308 DIRRCQTPNDRFTILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAADARYEAA- 366
DB 212 DVVVHEITDDDEFVLVACDGIWDCKTSQVIEFV-----RGIIVAGTSLEKIAE 260

QY 367 ---CNRLANKAVQSG--SADNVTVMVVRI 390
DB 261 NLMDCIASDTETTLGLCDNNTVCIVAL 288

RESULT 5
T05095
hypothetical protein F28M20.60 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Jun-2001
C:Accession: T05095
R:Bevan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Hoheisel, J.; Mewes, submitted to the Protein Sequence Database, November 1998
A:Reference number: Z15398
A:Accession: T05095
A:Molecule type: DNA
A:Residues: 1-389 <BEV>
A:Cross-references: EMBL:AL031004
A:Experimental source: cultivar Columbia; BAC clone F28M20
C:Genetics:
A:Map position: 4
A:Introns: 95/1; 128/1; 181/1; 210/1; 274/3; 318/3
A:Note: F28M20.60
C:Superfamily: human phosphoprotein phosphatase 1A

Query Match 18.2%; Score 368; DB 2; Length 389;
Best Local Similarity 33.7%; Pred. No. 2.1e-19;
Matches 114; Conservative 40; Mismatches 86; Indels 98; Gaps 14;

QY 109 GYVAERGEREEMQDAHVILNDITECRPPSLITRVSYFAVFDGHHGIRASKFAAQNLH 168
DB 60 GY-ASSPKGRSMEDFYETRIDGVEG-----EIVGLFVGFDGHHGARAAYVKONLF 110

QY 169 QNLIRKFPKGDVISVEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKD--GSTATCVLAVDN 227
DB 111 SNLIR-HPK--FIS---DTTAAIADAYNQTDSEFLKNSQN---RDAGSTASTAILVGD 161

QY 228 ILYIANLGDRAILCRNEESQKHAALSLSKEHNPQYEEERMRIQKAGNV---DGRVL 284
DB 162 RLLVANVGDSSRAVICRGN-----ATAVSRDKPQDSERQRIEDAGGFVWAGTWVVG 215

QY 285 GVLEVSRSIGDGQYKRCGVTSVPDIR----- 310
DB 216 GVLAVSRAFGDRLLKQY--VWADPETQVLTFCQNLVKNATLLTIEHNLHWSIVSYL 274

QY 311 -----RCQLTPNDR-----FILLACDGLFKVFTPEEAVNFILSCLEDEKIQ 351
DB 275 NGTLQNFRLRSLTSINGKFOEKVPSSEFLILASDGLWDVVVNSNEEAVGMI--KATIEDP--- 330

QY 352 TREGKSAADARYEAACNLANKAVQSGADNVTVMVVRI 389
DB 331 -----EAGAKLMEAVQSGADNITCVVVR 356

RESULT 6
T08606
protein phosphatase 2C-like protein Spalten - slime mold (Dictyoetelium discoideum)
C:Species: Dictyoetelium discoideum
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C:Accession: T08606
R:Aubry, L.; Firtel, R.A.

Db 112 PFDVSPFEASELDEIFUE-GVENCRLRAFFLAD---LALADDCSISTSGTALTALV 167
Qy 225 VDNILYIANLGSRAILCRYNEESOKHAALSKEHNPTQYEERMRIQKAGNVRDGRVL 284
Db 168 LGRLLIVANAGDRAVLCKGE-----AIDNSQDHRFTYPEKRVVEELGGYVDDGYLN 221
Qy 285 GVLEVSRSIGDQYK-----RCGVTSVPDIRRCQLTDPNDRFILLACDGLFKVFTPEEAVN 339
Db 222 GVLVSRAIGDMDKLPKGSAPLISEPELRQIILTEDDEFLIIGCDGIWDVSSQQAVS 281
Qy 340 FILSCLEDEKIOTREGSKAADARYEAACNRLANKAVQGSADNVTVMVV 388
Db 282 IV-----RWGLKXHDPP-EQSAKDLVNEALRRHTDNLTLIV 318

RESULT 8
T50783
protein phosphatase 2C-like protein - Arabidopsis thaliana
N:Alternate names: protein T30N20.10
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 15-Jun-2001
C:Accession: T50783
R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirksee, W.; Stiekema, W.; Bancroft, I.; Mew
submitted to the Protein Sequence Database, July 2000
A:Reference number: Z25240
A:Accession: T50783
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-348 <BEV>
A:Cross-references: EMBL:AL365234
A:Experimental source: cultivar Columbia; BAC clone T30N20
C:Genetics:
A:Map position: 5
A:Introns: 27/2; 70/1; 103/1; 156/1; 185/1; 209/3; 234/3
A:Note: T30N20.10
C:Superfamily: human phosphoprotein phosphatase 1A

Query Match 18.1%; Score 364.5; DB 2; Length 348;
Best Local Similarity 36.4%; Pred. No. 3.2e-19;
Matches 103; Conservative 47; Mismatches 86; Indels 47; Gaps 13;
Qy 109 GYVAERKGEREEMQD-AHVILNDITECPSPSLITRVSFAVFDGHHGIRASKFAQNL 167
Db 35 GY-ASSAGKRSSNEDFFETRIDGNGEI-----VGLFGVFDGHHGARAAYVKRHL 84
Qy 168 HQNLIRKPKGDVISVEKTVKRCCLDTFKHTDEEFLKQASSOKPAWKD-GSTATCVLAVD 226
Db 85 FSNLI-THPK--FIS--DTKSAITDAYNHTDSSELLKSENHN---RDAGSTASTAILVG 135
Qy 227 NILYIANLGSRAILCRYNEESOKHAALSKEHNPTQYEERMRIQKAGNVRDGRVLGV 286
Db 136 DRUVANVAGDSRAVISRGKK-----AIAVSRDHKPDQSDERERENAGGFV---MWAGV 186
Qy 287 LEVSRSIGDQYKRCGVTSVPDIRRCQLTDPNDRFILLACDGLFKVFTPEEAVNFILSCLE 346
Db 187 LAVSRAFGRLKQY-VVADPEIQEIKDICTLEFLILASDGLWDVFSNEAAVAVV----- 240
Qy 347 DEKIOTREGSKAADARYEAACNRLANKAVQGSADNVTVMVV 389
Db 241 -----KEVEDP--EDSAKLVGEAIKRGSAADNITCVVVR 272

RESULT 9
H96700
protein F12A21.5 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: H96700
R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H96700
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-464 <STO>
A:Cross-references: GB:AE005173; NID:gl1072032; PIDN:AAG28911.1; GSPDB:GN00141
C:Genetics:
A:Gene: F12A21.5
A:Map position: 1

Query Match 17.9%; Score 362; DB 2; Length 464;
Best Local Similarity 29.3%; Pred. No. 7.3e-19;
Matches 108; Conservative 59; Mismatches 104; Indels 98; Gaps 13;
Qy 102 SVIFGLKGY-VARKGEREEMQDAHVILNDITECPSPSLITRVSFAVFDGHHGIRAS 160
Db 113 TVSFGGNGFGWGRNGKKFMEDTHRIV-----PCLVGNSS---KGSFFGVYDGHGAKAA 164
Qy 161 KPAQNHLQNLIRKFP--KGDVISVEKTVKRCCLDTFKHTDEEFLKQASSOKPAWKDGST 218
Db 165 EFVAENLHYVVMENCKGEEKVE-----AFKAAFLTRDRLDFLEKVKTEQSLKGVVSG 219
Qy 219 ATCVLAV--DNILYIANLGSRAILCRYNEESOKHAALSKEHNPTQYEERMRIQK--- 273
Db 220 ACCVTAVIQDEMIVSNLGCRAVLCRAG-----VAEALTDDKFCRDEKERISQS 273
Qy 274 -----AGGNVRD---GRVLGVLEVSRSIGDQYKRCGVTSVPDIRRCQLTDPNDRFI 321
Db 274 IPFWTFGLQGYVDNHQGAWRVQGVILAVSRSIGDAHLKK-WVAEPETRVLELEQDMEFL 332
Qy 322 LLACDGLFKVFTPEEAVNFILSCJ-----EDEKIQ-----TREG 355
Db 333 VLASDGLWDVSNQEAAYTVLHVAQRKTPKESEENLVQGFVNMSPSSKLRLASLVKSP 392
Qy 356 KSAADARY-----EAAACNRLANKAVQGSADNV 383
Db 393 RCASKQSYYYNSNESPSLNREITGSSFSKSPITFWKSLMAKAAACKELANLAKRGSMDDI 452
Qy 384 TVMVVRIGH 392
Db 453 TVVIIDLNH 461

RESULT 10
T45778
protein phosphatase 2C-like protein - Arabidopsis thaliana
N:Alternate names: protein F26013.110
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 03-Jun-2002
C:Accession: T45778
R:Delseray, M.; Berger, C.; Cooke, R.; Grellet, F.; Laudie, M.; Mewes, H.W.; Lemcke, K.;
submitted to the Protein Sequence Database, December 1999
A:Reference number: Z23013
A:Accession: T45778
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-361
A:Cross-references: EMBL:AL133452
A:Experimental source: cultivar Columbia; BAC clone F26013
C:Genetics:
A:Map position: 3
A:Introns: 49/3; 108/3
A:Note: F26013.110
C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.220

Query Match 17.8%; Score 358.5; DB 2; Length 361;
Best Local Similarity 30.6%; Pred. No. 9.4e-19;
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H96700
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-361
A:Cross-references: EMBL:AL133452
A:Experimental source: cultivar Columbia; BAC clone F26013
C:Genetics:
A:Map position: 3
A:Introns: 49/3; 108/3
A:Note: F26013.110
C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.220

RESULT 13

F84650
probable protein phosphatase 2C [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 01-Mar-2002
C;Accession: F84650
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84650
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-392 <STO>
A;Cross-references: GB:AE002093; NID:g4874313; PIDN:AAD31375.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g25620
A;Map position: 2
C;Superfamily: Arabidopsis thaliana hypothetical protein F7A7.220

Query Match 17.4%; Score 352; DB 2; Length 392;
Best Local Similarity 27.8%; Pred. No. 3.1e-18;
Matches 110; Conservative 73; Mismatches 152; Indels 60; Gaps 13;

QY 7 LPPEPRPRPAAGKEAQQGKLLFDLPPASSTDSGGGFLFDLPASSGDSGLATSI 66
DB 7 LSPDENGSSYGGK--PNNPLSF-----SSSAAAAYVQTFDGERSLAPCKSLVRH- 58
QY 67 SOMVTEGKAKRTS-BEEKNGSELVEKVKVCASSVIFLKGVAERKGEREEMODAH 125
DB 59 SSVLVKTMVSDISVENEFTIEKNKSEFVPATRGAMSDI-----GSRSSMEDAY 106
QY 126 VLINDITECPSPSLITRVSVFAVFDGGGIRASKFAQNLHQNLI--RKFPKGDVTSV 183
DB 107 LCVDFMDSFGLNLSEAGSFAYGFDGGHGKGAABFACHIPRYTIVEDQEPF----- 159
QY 184 EKVTKRCLDTFKHTDEEFLLQASQKPAWKDGTATCVLAVDNILYANLGDRAILCR 243
DB 160 -SEINKVLSAFLQDTAFL-EACSLDGLASGTTALAAIFGSLVVAAGDCRAVLSR 217
QY 244 YNEESQKHAALSLSKEHNPTOYERMRIQKAGNVDRGRVLGVLEVSRSIGD----QQYK 299
DB 218 QGK-----AIEMSRDHKPMSSKERRIEASGSHVFDGVLNGLNVAALGDFHEGK 271
QY 300 R-----CG-VTSVPDIRCOLTPNDRPFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTR 353
DB 272 KKGSDGCGPLIAEPELMTTKLTEDEFLLIGCDGVDVFMQSNVAFARRRLQSHNDPVM 331
QY 354 EGKSAADARYEACNPLANKAVQGSADNVTVMVV 388
DB 332 CSK-----ELVEEALKRKSSADNVTVAVV 354

RESULT 14

T00750
probable protein phosphatase 2C [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein T20B5.6
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Feb-2001
C;Accession: T00750; G84834
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,
submitted to the EMBL Data Library, November 1997
A;Description: Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence.
A;Reference number: Z14159
A;Accession: T00750
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-404 <ROU>
A;Cross-references: EMBL:AC002409; NID:g2623294; PID:g2623300
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: G84834
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-404 <STO>
A;Cross-references: GB:AE002093; NID:g2623300; PIDN:AAB86446.1; GSPDB:GN00139
C;Genetics:
A;Gene: T20B5.6; At2g40860
A;Map position: 2
A;Introns: 178/1; 200/2; 273/3; 308/3; 340/3

Query Match 17.4%; Score 351; DB 2; Length 404;
Best Local Similarity 29.3%; Pred. No. 3.9e-18;
Matches 110; Conservative 56; Mismatches 117; Indels 92; Gaps 13;

QY 65 SISQVMKTEGK---AKRTSEENKNGSE-----ELVEKKVKCASSV 103
DB 59 SIWEQVRGKQGHLEKTSNSQSDTDGADIKNSGDYRDTVNVWFSGQECLSKK--SSVST 116
QY 104 IFGLKCYVAERK-----GEEEMQDAHVILNDITEECRPPSSLITRVS 146
DB 117 VFDVKLWSSSTDEPSRYVPVISCGFATCGRESMEDTHFIIPMCNE-----ESIH 168
QY 147 YFAVFDGGHGIIRASKFAQNLHQNLIIRPKPKGDVTSVEKT-VKRCILDTFKHTDEEFLLQ 205
DB 169 LFAIFDGHGAAAFSAQVL-----PGLVSLCSTSAEALSOAFVTDLAFRQE 219
QY 206 ASSQKFA-----WKDGSATATCVLAVDNILYANLGDRAILCRYNESQKHAALSLSK 258
DB 220 LSHRQSKRVSKQKWHPGCTATASLLVENKLFVANVGDSRAILCRAGH-----PFALSK 273
QY 259 ENPTOYERMRIQKAGNVR-----DGRVLGV-LEVSRSIGDQYKRCQVTSVPDIRRQ 313
DB 274 AHLATCIDERNVIGEGRIEVLVDTWRVAPAGLQVTRSIGDDDLKP-AVTAPEISETI 332
QY 314 LTPNDFEILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAADARYEACNPLANK 373
DB 333 LSADDFLVNAGSLVMDVNDSEVIGIIRDTVKPESMCKS-----RLATE 377
QY 374 AVQGSADNVTVMVV 388
DB 378 AAARGSGDNITVIVV 392

RESULT 15

T06308
protein phosphatase 2C homolog F11C18.60 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 15-Jun-2001
C;Accession: T06308
R;Bevan, M.; Terry, N.; Ardiles, W.; Buyssehaert, C.; Dasseville, R.; De Clerck, R.; De
ewes, H.W.; Mayer, K.F.X.; Schueller, C.
submitted to the Protein Sequence Database, April 1999
A;Reference number: Z15589
A;Accession: T06308
A;Molecule type: DNA
A;Residues: 1-357 <BEV>
A;Cross-references: EMBL:AL049607; GSPDB:GN00062; ATSP:F11C18.60
A;Experimental source: cultivar Columbia; BAC clone F11C18
C;Genetics:
A;Gene: ATSP:F11C18.60
A;Map position: 4
A;Introns: 39/3; 61/1; 97/2; 148/3; 190/3; 232/1; 257/3; 275/2; 293/3
C;Superfamily: human phosphoprotein phosphatase 1A

Query Match 17.3%; Score 350; DB 2; Length 357;
Best Local Similarity 28.5%; Pred. No. 3.9e-18;
Matches 95; Conservative 59; Mismatches 95; Indels 84; Gaps 11;

QY	111	VAERGEREBEMODAHVINDITECRPSSILITRVSYFAVFDDHGGRASKFAAQNHLON	170
Dd	26	LSSMGWRASMEDAAHLLDLD-----NTSFLGYVDGGGWKSKFCAKYLHQO	75
QY	171	LI--RKFPKGQV-ISEVTXRCLLDTFKHTDEEFLQA-----	206
Dd	76	VUSDRAAGADVGTSLQKAFFR--WDMNQQRGRELAVLGDKINKFGSMIEGLIWSPR	133
QY	207	----SSOKP-AW-----KDGSTACVLADVNILYIANLGDSEAILCRYNESQ	249
Dd	134	SGDSANKPDWAPEBPGSHSDPAGNSGSTACVAVVRDKQLFVANAGDSRCVI-----SR	187
QY	250	KHAALSKEHNPTOYBERMIQKAGGNVRDGRVLGVLEVSRSIGDQYKRQG-----	302
Dd	188	KNOYNLSRDHKDPDLAEKERILKAGGFIAHAGRVNGSLNLSRAIGDMWFKNKFLPSEKQ	247
QY	303	-VTSVPDTRCOOLTENDRFILLACDGLVKVFTPEEAENVFILSCLEBEKITQTREGKSADA	361
Dd	248	I V T A S P D V N T V E L C D D D F L V L A C D G I W D C M T S Q O L V D F I H E Q L N S E -----T	295
QY	362	RVEAACNLANKAVORGA-----DNVTVMVVR	389
Dd	296	KLSUVCEKYLDRLCLAPNTSGEGGCDNMTHLVR	328

Search completed: April 12, 2004, 09:07:15
Job time : 22 secs

OM protein - protein search, using sw model

Run on: April 12, 2004, 09:01:42 ; Search time 17 Seconds
(without alignments)
1200.677 Million cell updates/sec

Title: US-09-935-124A-2

Perfect score: 2018

Sequence: 1 MDLFGDLPEPERSPPAAGK.....KAVQGSADNVTVMVRIGH 392

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	401.5	19.9	300	1 P2C PARTE	P49444 paramonium
2	370.5	18.4	414	1 P2C3 SCHPO	Q09173 schizosacch
3	366.5	18.2	454	1 FEM2 HUMAN	P49593 homo sapien
4	352.5	17.5	434	1 P2C1 ARATH	P49597 arabidopsis
5	348	17.2	370	1 P2C2 SCHPO	Q09172 schizosacch
6	347	17.2	356	1 P2C2 CAEEL	P49596 caenorhabdi
7	342	16.9	382	1 P2CA BOVIN	O62829 bos taurus
8	341.5	16.9	450	1 FEM2 RAT	O9WV7 rattus norv
9	340	16.8	382	1 P2CA RABIT	P35814 cryptolagus
10	340	16.8	382	1 P2CA RAT	P20650 rattus norv
11	338	16.7	382	1 P2CA MOUSE	P49443 mus musculu
12	336	16.7	382	1 P2CA HUMAN	P35813 homo sapien
13	333	16.5	423	1 P2C2 ARATH	O04719 arabidopsis
14	326	16.2	390	1 P2CB MOUSE	P36993 mus musculu
15	319	15.8	390	1 P2CB RAT	P35815 rattus norv
16	317.5	15.7	281	1 P2C1 YEAST	P35182 saccharomyc
17	314	15.6	387	1 P2CB BOVIN	O62830 bos taurus
18	313	15.5	479	1 P2CB HUMAN	O75688 homo sapien
19	306	15.2	347	1 P2C1 SCHPO	P40371 schizosacch
20	305.5	15.1	464	1 P2C2 YEAST	P39966 saccharomyc
21	305	15.1	388	1 P2C3 ARATH	P49599 arabidopsis
22	300	14.9	491	1 P2C1 CAEEL	P49595 caenorhabdi
23	289	14.3	468	1 P2C3 YEAST	P34221 saccharomyc
24	282.5	14.0	399	1 P2C4 ARATH	P49598 arabidopsis
25	271.5	13.5	405	1 P2C LEICH	P36982 leishmania
26	269.5	13.4	542	1 P2C3 MOUSE	O61074 mus musculu
27	267.5	13.3	393	1 P2C4 YEAST	P38089 saccharomyc
28	264	13.1	449	1 FEM2 CAEEL	P49594 caenorhabdi
29	256.5	12.7	543	1 P2CG BOVIN	P79126 bos taurus
30	255.5	12.7	546	1 P2CG HUMAN	O15355 homo sapien
31	211.5	10.5	2493	1 CYAA USTMA	P49606 ustilago ma
32	211	10.5	605	1 P2CD HUMAN	O15237 homo sapien
33	209	10.4	538	1 PDP1 BOVIN	P35816 bos taurus

34	209	10.4	598	1 P2CD MOUSE	Q9QZ67 mus musculu
35	208	10.3	2300	1 CYAA_NEUCR	O01631 neurospora
36	207	10.3	538	1 PDP1 RAT	O88483 rattus norv
37	206	10.2	1839	1 CYAA_SACKL	P23466 saccharomyc
38	204.5	10.1	383	1 P2C4 SCHPO	O14156 schizosacch
39	203	10.1	538	1 PDP1 HUMAN	Q9PCJ1 homo sapien
40	202	10.1	581	1 KAPP_ARATH	P46014 arabidopsis
41	194	9.6	529	1 PDP2 HUMAN	Q9P2J9 homo sapien
42	188	9.3	530	1 PDP2 RAT	O88484 rattus norv
43	185.5	9.2	2026	1 CYAA_YEAST	P08678 saccharomyc
44	178	8.8	504	1 TAB1 HUMAN	Q15750 homo sapien
45	178	8.8	2145	1 CYAA_PODAN	Q01513 podospora a

ALIGNMENTS

RESULT 1

P2C PARTE	ID	P2C PARTE	STANDARD;	PRT;	300 AA.
AC	P49444;				
DT	01-FEB-1996 (Rel. 33, Created)				
DT	01-FEB-1996 (Rel. 33, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Protein phosphatase 2C (EC 3.1.3.16) (PP2C).				
OS	Paramonium tetraurelia.				
OC	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;				
OC	Paramonium.				
OX	NCBI_TaxID=5888;				
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RC	STRAIN=Stock 51;				
RC	MEDLINE=95105156; PubMed=7806499;				
RA	Klunpp S., Hanke C., Donella-Deana A., Beyer A., Kellner R.,				
RA	Pinna L.A., Schultz J.E.;				
RT	"A membrane-bound protein phosphatase type 2C from Paramonium				
RT	tetraurelia. Purification, characterization, and cloning."				
RL	J. Biol. Chem. 269:32774-32780(1994).				
CC	- FUNCTION: Enzyme with a broad specificity.				
CC	- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +				
CC	phosphate.				
CC	- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).				
CC	- SUBCELLULAR LOCATION: Membrane-bound.				
CC	- PTM: The N-terminus is blocked.				
CC	- SIMILARITY: Belongs to the PP2C family.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
CC	EMBL; Z36985; CAA85448.1; --				
DR	PIR; A55804; A55804.				
DR	HSSP; P35813; LAQG.				
DR	InterPro; IPR001932; PP2C-like.				
DR	InterPro; IPR000222; PP2C.				
DR	Pfam; PF00481; PP2C; 1.				
DR	SMART; SM00331; PP2C SIG; 1.				
DR	SMART; SM00332; PP2C; 1.				
DR	PROSITE; PS01032; PP2C; 1.				
DR	Hydrolase; Magnesium; Manganese; Membrane.				
FT	METAL 37 37 MANGANESE 1 (BY SIMILARITY).				
FT	METAL 38 38 MANGANESE 1 (BY SIMILARITY).				
FT	METAL 57 57 MANGANESE 1 AND 2 (BY SIMILARITY).				
FT	METAL 237 237 MANGANESE 2 (BY SIMILARITY).				
FT	METAL 289 289 MANGANESE 2 (BY SIMILARITY).				
SQ	SEQUENCE 300 AA; 33739 MW; BC0318B4FF724EC CRC64;				

Query Match 19.9%; Score 401.5; DB 1; Length 300;
Best Local Similarity 33.0%; Pred. No. 7.7e-22;

FEM2 HUMAN
ID FEM2 HUMAN STANDARD; PRT; 454 AA.
AC P49593; Q36P2; PRT; 454 AA.
DT 01-FEB-1996 (Rel. 33, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ca(2+)/calmodulin-dependent protein kinase phosphatase (EC 3.1.3.16)
DE (CaM-kinase phosphatase) (CaMKPase) (Partner of PIX 2) (hFEM-2)
DE (Protein phosphatase 1F)
DE (Protein phosphatase 1F)
GN PPM1F OR POP2 OR KIAA0015.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21570215; PubMed=11559703;
RA Tan K.M.L., Chan S.L., Tan K.O., Yu V.C.;
RT "The Caenorhabditis elegans sex-determining protein fem-2 and its
human homologues, hFEM-2, are Ca2+/calmodulin-dependent protein kinase
phosphatases that promote apoptosis.";
RL J. Biol. Chem. 276:44193-44202(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21853182; PubMed=11864573;
RA Koh C.G., Tan E.J., Manser E., Lim L.;
RT "The p21-activated kinase PAK is negatively regulated by POPX1 and
POPX2, a pair of serine/threonine phosphatases of the PP2C family.";
RL Curr. Biol. 12:317-321(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Bone marrow;
RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,
Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
RT "Prediction of the coding sequences of unidentified human genes. I.
The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by
analysis of randomly sampled cDNA clones from human immature myeloid
cell line KG-1.";
RL DNA Res. 1:27-35(1994).
CC -!- FUNCTION: Dephosphorylates and concomitantly deactivates Cam-
kinase II activated upon autophosphorylation, and Cam-kinases IV
and I activated upon phosphorylation by Cam-kinase kinase.
CC Promotes apoptosis.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
phosphate.
CC -!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
CC -!- SUBUNIT: Associates with F1Aalpha.
CC -!- SIMILARITY: Belongs to the PP2C family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/>
or send an email to license@ebi.ac.uk).
CC
DR EMBL; AF305840; AAL15579.1; -;
DR EMBL; AF520615; AAM76059.1; -;
DR EMBL; D13640; BAA02803.1; -;
DR Genew; HGNC:19388; PPM1F.
DR InterPro; IPR001932; PP2C-like.
DR InterPro; IPR000222; PP2C.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR SMART; SM00332; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydrolase; Magnesium; Manganese; Apoptosis; Multigene family.
FT DOVAIN 101 107 POLY-GLU.
FT METAL 360 360 MANGANESE 2 (BY SIMILARITY).
FT METAL 404 404 MANGANESE 2 (BY SIMILARITY).
FT CONFLICT 202 202 G -> D (IN REF. 1).

SQ SEQUENCE 454 AA; 49830 MW; 2B49262333D4C9CF CRC64;
Query Match 18.2%; Score 366.5; DB 1; Length 454;
Best Local Similarity 28.3%; Pred. No. 4.5e-19;
Matches 127; Conservative 65; Mismatches 145; Indels 111; Gaps 16;
QY 10 PERSRPAPGAKEAQKPL--LFDDLPASSTDSGGPGLLFDLPASSGD-----SG 60
DB 6 PQKSPMASGAETPGFLDTLLQDPALLNPE-----DPLFWKAPGTVLQSQEEVEG 56
QY 61 SLA-----TSISQMVKTE-----GKAKAKTSEKXNGSEELVE 94
DB 57 ELAELAMGFLGSRKAPPPLAALAHAQVSLQTLSEFRKLPRSEEEEDDEEEKAP 116
QY 95 KKVCKASSVIFGLKGVVAERKCE-----RESMQDAHVIL 128
DB 117 VTLLDAQSLAQFFNRLMEVAGQKQVPLAARASQOWLSVHAIKNTRRKXDRHVS 176
QY 129 NDITECRPPSLITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRK-----PPKGDVISV 183
DB 177 PSF-NQLFGLSDPVR-AYFAVFDGHHGVDAAARYAAHVHTNAARQPELPTDEG----- 229
QY 184 EKTVRKCLLDTPKHTDEEFLKQASSQKPAWKGSTATCVLAVDNILYIANLGDSRAILR 243
DB 230 -----ALREAFRTDQWFLKAKRER--LQSGTTGVCAIAGATLHVAWLGDQVILV 280
QY 244 YNEESQKHAALSLSKEHNPTQYERVRQKAGNVRD---GRVLGVLEVSRSIGDQVYR 300
DB 281 -----QQGQVVKLMEPHPRQDERKARIEALGGFVSHMDCMRVNGTFLAVSRAIGD-VFOK 334
QY 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVTPPEANVNFILSCLEDEKIQREGKSAAD 360
DB 335 PYVSGEADAASRALTGSEDIYLLACDGFDDVVPVHGVVGLVQSHL-----TRQOGSLR 388
QY 361 ARVERACNELANKAVQSGADNVTVWV 388
DB 389 VAE-----LVAARERGHSDNITWV 411
RESULT 4
P2C1_ARATH STANDARD; PRT; 434 AA.
ID P2C1_ARATH STANDARD; PRT; 434 AA.
AC P49597; Q43717; Q94C87;
DT 01-FEB-1996 (Rel. 33, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Protein phosphatase 2C ABI1 (EC 3.1.3.16) (PP2C) (Abscissic acid-
insensitive 1).
DE Insensitive 1).
GN ABI1 OR AT4G26080 OR F20B18.190.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT ASP-180.
RC STRAIN=cv. Landsberg erecta;
RX MEDLINE=94255767; PubMed=8197457;
RA Meyer K., Leube M.P., Grill E.;
RT "A protein phosphatase 2C involved in ABA signal transduction in
Arabidopsis thaliana.";
RL Science 264:1452-1455(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia; TISSUE=Leaf;
RX MEDLINE=95007758; PubMed=7923358;
RA Mindrinos M., Katagiri F., Yu G.L., Ausubel F.M.;
RT "The A. thaliana disease resistance gene RP2 encodes a protein
cell wall 78:1089-1099(1994).
RL [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia; TISSUE=Leaf;

QY 384 TVMVV 368
Db 416 SVVVV 420

RESULT 5
P2C2_SCHPO STANDARD; PRT; 370 AA.
AC Q09172;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein phosphatase 2C homolog 2 (EC 3.1.3.16) (PP2C-2).
GN P2C2 OR SPCC1223.11.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=972;
RC MEDLINE=95163582; PubMed=7859738;
RX RA Shiozaki K., Russell P.;
RT "Counteractive roles of protein phosphatase 2C (PP2C) and a VAP
RL kinase homolog in the osmoregulation of fission yeast.";
RL EMBO J. 14:492-502(1995).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=972;
RC MEDLINE=21848401; PubMed=11859360;
RX RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Baeham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squires A., Walsh S.V., Warren T., Whitehead S.,
RA Taylor K., Taylor R.G., Tivey A.R., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Art R., Robben J., Gymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goifeau A., Cadieu E., Drano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- FUNCTION: Has an important role in osmotic stability and cell
CC shape control. It may negatively regulate the osmosensing signal
CC transmitted through wsl map kinase.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: Belongs to the PP2C family.
CC
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CC EMBL; L34881; AAA67320.1; -.
DR EMBL; AL031579; CAA20880.1; -.
DR PIR; S54297; S54297.
DR HSSP; P35813; 1A6Q.
DR GeneDB SPombe; SPCC1223.11; -.
DR InterPro; IPR001932; PP2C-like.
DR InterPro; IPR000222; PP2C.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00331; PP2C SIG; 1.
DR SMART; SM00332; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydrolase; Magnesium; Manganese; Multigene family.
FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
FT METAL 63 63 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL 233 233 MANGANESE 2 (BY SIMILARITY).
FT METAL 282 282 MANGANESE 2 (BY SIMILARITY).
SQ SEQUENCE 370 AA; 40878 MW; DBDDB826F440AC50 CRC64;
Query Match 17.2%; Score 348; DB 1; Length 370;
Best Local Similarity 32.5%; Pred. No. 7.3e-18;
Matches 98; Conservative 47; Mismatches 103; Indels 54; Gaps 12;
QY 111 VAERKGEREEMQDAHVILNDITE--ECRPSSLTIRVSYPAVFDHGHGIRASKFAAQNLIH 168
Db 26 VSHMQGWRISMEDAHCALLNFTDSNSNPPT-----SFFGVFDHGHGDRVAKYCRQHL- 78
QY 169 QNLIRKFP---KGDVISVEKTVKRCLLDTFKHTDEEFLKQASSOKPAWKDGTATCVLAV 225
Db 79 PDIIKQSQSFWKGN-----YDEALKSGFLAANALMQDRMQED--PSGCTATALLIV 129
QY 226 DN-ILYIANLGDRAILCRVNEESOKHAALSLSKEHNPTQYEERMRIQAGNVDRGRVL 284
Db 130 DQVITYCANAGDSRVILGR-----KGTAEPLSPDKPNNDVEKARITAGGDFIDGRVN 183
QY 285 GYLEVSRSIGDQYKRCG-----VTSVPDIRCQLTPNDRFILLACDGLFKVFTPEE 336
Db 184 GSLALSRAIGDPEYKKSLSLPEKQIVTAFDVIHNDPDDDEFILACDGTWCKSSQQ 243
QY 337 AVNFIKLEDEKIQTRGKGAADARYAACNRLANKAVQRGS-----ADNVTVWVYRI 390
Db 244 VVEFY-----RRGIVARQS-LEVICENLMDRCIASNESCIGICDNTTICIVAF 291
QY 391 GH 392
Db 292 LH 293
RESULT 6
P2C2_CABEL STANDARD; PRT; 356 AA.
ID P2C2_CABEL
AC P49596;
DT 01-FEB-1996 (Rel. 33, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable protein phosphatase 2C T23F11.1 (EC 3.1.3.16) (PP2C).
GN T23F11.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RC STRAIN=Bristol N2;
RA Swinburne J.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP REVISIONS.
RA Durbin R.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.

CC -1- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
 CC -1- SIMILARITY: Belongs to the PP2C family.
 CC
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 CC
 CC EMBL: Z46343; CA48456.2; -
 CC FIR; T25181; T25181.
 CC DR WormPep; T23F11.1; CE24009.
 CC DR InterPro; IPR001932; PP2C-like.
 CC DR InterPro; IPR000222; PP2C.
 CC DR Pfam; PF00481; PP2C; 1.
 CC DR SMART; SM00331; PP2C_Sig; 1.
 CC DR SMART; SM00332; PP2C; 1.
 CC DR PROSITE; PS01032; PP2C; 1.
 CC KW Hypothetical protein; Hydrolase; Magnesium; Manganese.
 CC FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
 CC FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
 CC FT METAL 59 59 MANGANESE 1 AND 2 (BY SIMILARITY).
 CC FT METAL 228 228 MANGANESE 2 (BY SIMILARITY).
 CC FT METAL 277 277 MANGANESE 2 (BY SIMILARITY).
 CC SQ SEQUENCE 356 AA; 39064 MW; EDCB0841CFB026B5 CRC64;
 CC
 CC Query Match 17.2%; Score 347; DB 1; Length 356;
 CC Best Local Similarity 31.4%; Pred. No. 8.2e-18;
 CC Matches 101; Conservative 57; Mismatches 108; Indels 56; Gaps 12;
 CC
 CC QY 91 ELVEKKVKASSVIGLKGVAE---RKGEREMQDAHVILNDITECRPPSSLIITVSVY 147
 CC DB 3 QTLSEPVTKESASCANENLYVGSSCQGVWRVDEDAHTLLSLPDD-----PKCAF 54
 CC
 CC QY 148 RAVFDGHGGIRASKEFAAONLHNL--RKFKPGDV-ISVEKTVKRLDTEKHTDEBFLK 204
 CC DB 55 RAVFDGHGGKSVQSGINLHKVVAQKEFEGNKEAIEKGFLE--LDQQRVDEBTKD 112
 CC QY 205 QASSQKPAWKDGSTATCVLAVDNILYIANLGDSRAILCRYNESQKHAALSLSKEHNPTQ 264
 CC DB 113 DVS-----GTTAVVVLKEGDVYCGNAGDSRAVSSVSGE-----ARPLSPDHKPSH 158
 CC QY 265 YERWRIQKAGNVDRGRVLGVLEVSRSIGDQYKRCG-----VTSVPDIRCQLTTP 316
 CC DB 159 ETEARRITAAAGGWFEFNRVNGNLALSRAIGDPFAFKNCDTKPAEQIVTAFDPDVTDKLTP 218
 CC QY 317 NDRFILLACDGLFKVFTPEBAVNFILSCLEDEKIQTRREGKSAADARYEAACNRLANKAV- 375
 CC DB 219 DHEFIVLACDGIWDVMTNQEVVDFV-----RE-KLAEKDPQSCIEELLTRCLA 266
 CC QY 376 ---QRG--SADNVTVWVRIGH 392
 CC DB 267 PQCQGGGLGCDNVTVLVGLLH 288
 CC
 CC RESULT 7
 CC P2CA_BOVIN
 CC ID_P2CA_BOVIN STANDARD; PRT; 382 AA.
 CC AC O62829;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha).
 CC GN PPM1A.
 CC OS Bos taurus (Bovine).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC OC Bovidae; Bovinae; Bos.
 CC OX NCBI_TaxID=9913;
 CC RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=98146173; PubMed=9486768;
 RA Klump S., Selke D., Fischer D., Baumann A., Mueller F., Thanos S.;
 RT "protein phosphatase type-2C isoforms present in vertebrate retinae;
 RT purification, characterization, and localization in photoreceptors.";
 RL J. Neurosci. Res. 51:328-338(1998).
 CC -1- FUNCTION: Enzyme with a broad specificity.
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -1- COFACTOR: Binds 2 magnesium or manganese ions.
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SIMILARITY: Belongs to the PP2C family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AJ005457; CAA06554.1; -
 CC HSP; P35813; IAGQ.
 CC DR InterPro; IPR001932; PP2C-like.
 CC DR InterPro; IPR000222; PP2C.
 CC DR Pfam; PF00481; PP2C; 1.
 CC DR SMART; SM00331; PP2C_Sig; 1.
 CC DR SMART; SM00332; PP2C; 1.
 CC DR PROSITE; PS01032; PP2C; 1.
 CC KW Hydrolase; Magnesium; Manganese; Multigene family.
 CC FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
 CC FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
 CC FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
 CC FT METAL 239 239 MANGANESE 2 (BY SIMILARITY).
 CC FT METAL 282 282 MANGANESE 2 (BY SIMILARITY).
 CC SQ SEQUENCE 382 AA; 42529 MW; A716B3FA0E7E21C2 CRC64;
 CC
 CC Query Match 16.9%; Score 342; DB 1; Length 382;
 CC Best Local Similarity 33.7%; Pred. No. 2.1e-17;
 CC Matches 101; Conservative 47; Mismatches 104; Indels 48; Gaps 12;
 CC
 CC QY 106 GLGYVAERKGEREEMQDAHVILNDITECRPPSSLIITVSVFAPDGHGGIRASFAAQ 165
 CC DB 21 GLRYGLSSQGVREVEDAHTAVIGL-----PSGLET-WSFFAVYDGHAGSVAKYCC 73
 CC QY 166 NLHQNLIKRP-KGD--VISVEKTVKRLDTEKHTDEBFLKQASSQKPAWKDGSTATCV 222
 CC DB 74 HLLDHTNNQDFKSGAGAPSV-NVKNGITRTGFLDEHVRVMSKKHGGADRSSTAVGV 132
 CC QY 223 LAVDNILYIANLGDSRAILCRYNESQKHAALSLSKEHNPTQYERWRIQKAGNVDRGR 282
 CC DB 133 LISPOHTYFTNCGDSRGLICR-----NRKVYFTQDHRKPSNPLEKRIQAGGSVMIO 186
 CC QY 283 VLGVLEVSRSIGDQYKRC---GVT-----SVPDIRCQLTENDRIFILLACDGLFK 330
 CC DB 187 VNGSLAVSRALGDFDYK-CVHGKGPTEQLVSPPEVHDIERS-EDDQFIILACDGIWD 243
 CC QY 331 VFTPEAVNFILSCLE--DEKIQTRREGKSAADARYEAACNRLANKAVQSGADNVTVWV 388
 CC DB 244 VMGNEELCDFVRSRLVTD-----LEKVCNEVVDTCLYKGRDNMSVILI 289
 CC
 CC RESULT 8
 CC FEM2_RAT
 CC ID_FEM2_RAT STANDARD; PRT; 450 AA.
 CC AC Q9WV7;
 CC DT 28-FEB-2003 (Rel. 41, Created)
 CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE Ca(2+)/calmodulin-dependent protein kinase phosphatase (EC 3.1.3.16)
 CC DE (CaM-kinase phosphatase) (CaMKPase) (Partner of PIX 2) (Protein
 CC phosphatase 1P).

QY 327 GLFKVTPTEAVNFILSCLEDEKIQTRGKGAADARYEAACNRLANKAVQSGADNVTVM 386
Db 357 GFDFVPPHPIGVLGHLLRQK---GSGMHVAE-----ELVAVARDGRSHDNITVM 405
QY 387 VV 398
Db 406 VV 407
RESULT 9
P2CA_RABIT STANDARD; PRT; 382 AA.
AC P35814;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha) (IA)
DE (Protein phosphatase 1A).
DE PPM1A OR PPM1A.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92182001; PubMed=1311954;
RA Mann D.J., Campbell D.G., McGowan C.H., Cohen P.T.W.;
RT "Mammalian protein serine/threonine phosphatase 2C: cDNA cloning and
RT comparative analysis of amino acid sequences.";
RL Biochim. Biophys. Acta 1130:100-104(1992).
CC -!- FUNCTION: Enzyme with a broad specificity.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- COFACTOR: Binds 2 magnesium or manganese ions.
CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: Belongs to the PP2C family.
CC
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CC
CC EMBL; S87757; AAB21783.1; -.
DR PIR; S22422; S22422.
DR HSP; P35813; IAA60.
DR InterPro; IPR001932; PP2C-like.
DR InterPro; IPR000222; PP2C.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR SMART; SM00332; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydrolase; Magnesium; Manganese; Multigene family.
FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL 239 239 MANGANESE 2 (BY SIMILARITY).
FT METAL 282 282 MANGANESE 2 (BY SIMILARITY).
SQ SEQUENCE 382 AA; 42462 MW; 46SCF1854FDIC486 CRC64;
Query Match 16.8%; Score 340; DB 1; Length 382;
Best Local Similarity 33.7%; Pred. No. 2.9e-17;
Matches 101; Conservative 47; Mismatches 104; Indels 48; Gaps 12;
QY 106 GLGKYVAERKGEREEMQDAHVILNDITECRPPSSLIITVSVFVDPDGGGRASFAAQ 165
Db 21 GLAYGLSSMQGWRVEMEDAHTAVIGL-----PSGLET-WSFFAVYDGHAGSQVAKYCE 73
QY 166 NLHQNIRKPP-KGD--VISVEKTVKRCLLDTFKHTDEFLKQASSQKPAWKDGSTATCV 222

GN PPM1F OR POPX2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99279559; PubMed=10348902;
RA Kitani T., Ishida A., Okuno S., Takeuchi M., Kameshita I.,
RT "Molecular cloning of Ca2+/Calmodulin-dependent protein kinase
phosphatase.";
RL J. Biochem. 125:1022-1028(1999).
CC -!- FUNCTION: Dephosphorylates and concomitantly deactivates Cam-
CC kinase II activated upon autophosphorylation, and Cam-kinases IV
CC and I activated upon phosphorylation by Cam-kinase kinase.
CC Promotes apoptosis.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
CC -!- SUBUNIT: Associates with FlA1pha (By similarity).
CC -!- SIMILARITY: Belongs to the PP2C family.
CC
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CC
CC EMBL; AB023634; BAA82477.1; -.
DR InterPro; IPR001932; PP2C-like.
DR InterPro; IPR000222; PP2C.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR SMART; SM00332; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydrolase; Magnesium; Manganese; Apoptosis; Multigene family.
FT DOMAIN 99 109 POLY-GLU.
FT METAL 356 356 MANGANESE 2 (BY SIMILARITY).
FT METAL 400 400 MANGANESE 2 (BY SIMILARITY).
SQ SEQUENCE 450 AA; 49165 MW; 67626542F32B2FD0 CRC64;
Query Match 16.9%; Score 341.5; DB 1; Length 450;
Best Local Similarity 29.4%; Pred. No. 2.8e-17;
Matches 124; Conservative 63; Mismatches 160; Indels 75; Gaps 16;
QY 3 LFGDLPEPERSPPAAGKEAQKGPLLFDLPASSTDSGGGPLLFDLPASSGDSGL 62
Db 25 LLQDFPALSLESPLPWK--VPGTVLQGEVEAEITELAMGF-LGSRNAPAVA--AAVT 79
QY 63 ATSIQMYKTEKGAKRTSBEKNGSE-----LVEKK-----VCKASSVI 104
Db 80 HEAISQLQTLSEPKRLPEQEVEEERVLTLDAKGLSRFFNCLMEVCSQWQKR 139
QY 105 FLGKYVAERK-----GEREMQDAHVILNDITECRPPSSLIITRV8-----YEA 149
Db 140 VELTAQAPQKWLVSIAHRTNRKMDRHVSL-----PAPNHLFGLSDSVHRAYFA 191
QY 150 VFDGGGGRASFAAQNLHQNIRKPPKGDVTSVEKTVKRCLLDTFKHTDEFLKQASSQ 209
Db 192 VFDGGGVDAAIYASVHVTHNASHQ-PE-----LLTDPAAALKEAFHTDQMFQAKRE 245
QY 210 KPAWKDGSTATCVLAVDNIYLIYANGSRAILCRYNEESQKHAALSISKEINPTQYERM 269
Db 246 R--LQSGITGVCALLTGAAHVAWLGDSQVILV-----QQQVVKLMPEKPERQDEKS 297
QY 270 RIQKAGGNVR---DGRVJGVLEVSISGQVQKRGVTSVPDIRRCQTLPNDRILLACD 326
Db 298 RIEALGGFVSLMDCWRVNGTAVSAIGD-VFQKPYVSGEADAASRELTGLEDYILLACD 356

Qy 106 GLKGYVAERKGBREEMQDAHVILNDITEBCRPSSLIITVSYFNVFDHGGRASKFAAQ 165
 Db 21 GLRYGLSSMQGKRWEMEDAHVIGL-----PSGLT-WSFPAVYDGHAGSQVAKYCCB 73
 Qy 166 NLHQNLIRKFP-KGD--VISVEKTVKRCLLDTPKHTDEEFLKQASSQKPAWKDGGSTATCV 222
 Db 74 HLDHITNNQDFKSGAGAPSVB-NVKNIGRTGFLDEIDHMRVMSKKHGADRSSTAVGV 132
 Qy 223 LAVDNILYIANLGDRAILCRVNEESQKHAALSKEHNPTQYEEMRIOKAGNVDRGR 282
 Db 133 LISPQHTYFINGDSRGLLCLR-----NRKVHFFTDQHKFSPNLEKRIQAGGSVMIOQ 186
 Qy 283 VLGVLVRSISGQGYKRC-----GVT-----SVPDIRCOLTENDRIFILLACDGLFK 330
 Db 187 VNGSLAVSRALGDFDYK-CVHGKGPTEQLVSPPEVHDIERSE--EDDQFIILACDGIWD 243
 Qy 331 VTPPEAVNFIISLB--DEKIQTRGKSAADARVEAACLANKAVQGSADNVTVWV 388
 Db 244 VMGNEELCDFVRSRLVTD-----LEKVCNEVVDTCYKSGSRDNMSVILI 289

RESULT 11

F2CA MOUSE
 ID P2CA MOUSE STANDARD; PRT; 382 AA.
 AC P49443;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha) (IA)
 GN (Protein phosphatase 1A).
 GN PPM1A OR PPM1A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=94333828; PubMed=8056349;
 RA Kato S., Kobayashi T., Terasawa T., Ohnishi M., Sasahara Y.,
 RA Karamaru R., Tamura S.;
 RT "The cDNA sequence encoding mouse Mg2+ -dependent protein phosphatase
 RT alpha.";
 RL Gene 145:311-312(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed12477932;
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Kirschner A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RL human and mouse cDNA sequences.";
 CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Enzyme with a broad specificity.
 CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -!- COFACTOR: Binds 2 magnesium or manganese ions.
 CC -!- SUBUNIT: Monomer.
 CC -!- SIMILARITY: Belongs to the PP2C family.

Db 74 HLDHITNNQDFKSGAGAPSVB-NVKNIGRTGFLDEIDHMRVMSKKHGADRSSTAVGV 132
 Qy 223 LAVDNILYIANLGDRAILCRVNEESQKHAALSKEHNPTQYEEMRIOKAGNVDRGR 282
 Db 133 LISPQHTYFINGDSRGLLCLR-----NRKVHFFTDQHKFSPNLEKRIQAGGSVMIOQ 186
 Qy 283 VLGVLVRSISGQGYKRC-----GVT-----SVPDIRCOLTENDRIFILLACDGLFK 330
 Db 187 VNGSLAVSRALGDFDYK-CVHGKGPTEQLVSPPEVHDIERSE--EDDQFIILACDGIWD 243
 Qy 331 VTPPEAVNFIISLB--DEKIQTRGKSAADARVEAACLANKAVQGSADNVTVWV 388
 Db 244 VMGNEELCDFVRSRLVTD-----LEKVCNEVVDTCYKSGSRDNMSVILI 289

RESULT 10

F2CA RAT
 ID P2CA RAT STANDARD; PRT; 382 AA.
 AC P20650;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha) (IA)
 GN (Protein phosphatase 1A).
 GN PPM1A OR PPM1A OR PP2C1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=89184515; PubMed=2538815;
 RA Tamura S., Lynch K.R., Lerner J., Fox J., Yasui A., Kikuchi K.,
 RA Suzuki Y., Tsuki S.;
 RT "Molecular cloning of rat type 2C (IA) protein phosphatase mRNA.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:1796-1800(1989).
 CC -!- FUNCTION: Enzyme with a broad specificity.
 CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -!- COFACTOR: Binds 2 magnesium or manganese ions.
 CC -!- SUBUNIT: Monomer.
 CC -!- SIMILARITY: Belongs to the PP2C family.

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 CC or send an email to license@isb-sib.ch)

CC EMBL: J04503; AAA1917.1; --
 DR F1R; A32399; A32399.
 DR HSSP; P35813; 1A6Q.
 DR InterPro: IPR001932; PP2C-like.
 DR InterPro: IPR00222; PP2C.
 DR Pfam: PF00481; PP2C; 1.
 DR SMART; SM00331; PP2C SIG; 1.
 DR SMART; SM00332; PP2CC; 1.
 DR PROSITE; PS01032; PP2C; 1.
 DR Hydrolase; Magnesium; Manganese; Multigene family.
 FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
 FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
 FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL 239 239 MANGANESE 2 (BY SIMILARITY).
 FT METAL 282 282 MANGANESE 2 (BY SIMILARITY).
 SQ SEQUENCE 382 AA; 42416 MW; C1C386B935374F89 CRC64;

Query Match
 Best Local Similarity 33.7%; Pred. No. 2.9e-17;
 Matches 101; Conservative 47; Mismatches 104; Indels 48; Gaps 12;

CC -1- SIMILARITY: Belongs to the PP2C family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; D28117; BAA05662.1; -;
CC EMBL; BC008595; AA08595.1; -;
CC PIR; I53823; I53823.
CC HSP; P35813; IA6Q.
CC MGD; MGI:199878; Ppmla.
CC InterPro: IPR001932; PP2C-like.
CC InterPro: IPR000222; PP2C.
CC Pfam; PF00481; PP2C; 1.
CC SMART; SM00331; PP2C_SIG; 1.
CC PROSITE; PS01032; PP2C; 1.
CC PROSITE; PS01032; PP2C; 1.
CC Hydrolase; Magnesium; Manganese; Multigene family.
CC METAL 37 37 MANGANESE 1 (BY SIMILARITY).
CC METAL 38 38 MANGANESE 1 (BY SIMILARITY).
CC METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
CC METAL 239 239 MANGANESE 2 (BY SIMILARITY).
CC METAL 282 282 MANGANESE 2 (BY SIMILARITY).
CC SEQUENCE 382 AA; 42432 MW; DC206610E1583870 CRC64;
Query Match 16.7%; Score 338; DB 1; Length 382;
Best Local Similarity 33.0%; Pred. No. 4e-17;
Matches 99; Conservative 47; Mismatches 106; Indels 48; Gaps 11;
QY 106 GLKGYVAERGEREMQDAHVINDITECRPSSILITRVSYFAVDFGCGIRPASFQAQ 165
DB 21 GLRYGLSMQGWREMDAHTAVIGL-----PSGLET-WSFFAVYDGHAGSQVAKYCC 73
QY 166 NLHQLNRKFP---KGDVISVETKVRCLLDTFCHTDEEFLKQASSQKPAWKDGSATCV 222
DB 74 HLDHITNNQDFRSGAGAPSVENKMGIRTGFLFDEHVRVSEKXGHADRSSTAVGV 132
QY 223 LAVDNILYIANLGDRAILCRVNEESQKHAALSKEHNPTQYEERMRIQKAGNVRDGR 282
DB 133 LISQHYFFYFNGDSRGLCLR-----NRKVHFTQDKHPSNPLEKRIQAGSVMIQR 186
QY 283 VLGVLVRSIGDQYKRC-----SVDPDIRCOLTPNDFILLACDGLFK 330
DB 187 VNGSLAVSRALGDPDYK-CVHGKGPTEQLVSPPEVHDIERSE--EDDQFIILACDGIWD 243
QY 331 VFTPEEAVNFILSCLE--DEKIQREKSAADARYEAACHNLANKAVQSGADNVTVMVV 388
DB 244 VMGNEELCDFVRSLEVTDD-----LEKVCNEVVDTCLYKSGRDNMSVILI 289
RESULT 12
P2CA_HUMAN STANDARD; PRT; 382 AA.
AC P35813; 075551;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha) (IA)
DE (Protein phosphatase 1A).
GN PPM1A OR PPM1A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA-1).
RX MEDLINE=92182001; PubMed=1311954;
RA Mann D.J., Campbell D.G., McGowan C.H., Cohen P.T.W.;
RT "Mammalian protein serine/threonine phosphatase 2C: cDNA cloning and

RT comparative analysis of amino acid sequences.";
RL Biochim. Biophys. Acta 1130:100-104 (1992).
[2]
RN SEQUENCE FROM N.A. (ISOFORM ALPHA-2).
RX MEDLINE=98372738; PubMed=9707433;
RA Takekawa M., Maeda T., Saito H.;
RT "Protein phosphatase 2Calpha inhibits the human stress-responsive p38
RT and JNK MAPK pathways.";
RL EMBO J. 17:4744-4752 (1998).
[3]
RN SEQUENCE FROM N.A. (ISOFORM ALPHA-1).
RP TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[4]
RN X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE=97157470; PubMed=9003755;
RA Das A.K., Helps N.R., Cohen P.T.W., Barford D.;
RT "Crystal structure of the protein serine/threonine phosphatase 2C at
RT 2.0-A resolution.";
RL EMBO J. 15:6738-6809 (1996).
CC -1- FUNCTION: Enzyme with a broad specificity.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- COFACTOR: Binds 2 magnesium or manganese ions.
CC -1- SUBUNIT: Monomer.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha-1;
CC IsoId=P35813-1; Sequence=Displayed;
CC Name=Alpha-2;
CC IsoId=P35813-2; Sequence=VSP_005085, VSP_005086;
CC -1- SIMILARITY: Belongs to the PP2C family.
CC
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CC
CC -----
CC EMBL; S87759; AAB21784.1; -;
CC EMBL; AF070670; AAC28354.1; -;
CC EMBL; BC026691; AAH26691.1; -;
CC PIR; S22423; S22423.
CC Genew; HGNC:9275; PPM1A.
CC MIM; 606108; -;
CC PDB; 1AQJ; 27-MAY-98.
CC GO; GO:0015071; F:protein phosphatase type 2C activity; TAS.
CC InterPro; IPR001932; PP2C-like.
CC InterPro; IPR000222; PP2C.
CC Pfam; PF00481; PP2C; 1.
CC SMART; SM00331; PP2C_SIG; 1.

[illegible]

DR	HSP; P35913; 136Q.
DR	InterPro; IPR001932; PP2C-like.
DR	InterPro; IPR001932; PP2C.
DR	Pfam; PF00481; PP2C; 1.
DR	SMART; SM00331; PP2C SIG; 1.
DR	SMART; SM00332; PP2C; 1.
DR	PROSITE; PS01032; PP2C; 1.
DR	Hydrolase; Magnesium; Manganese; Multigene family; Calcium-binding.
KW	CA BIND 70 81 EF-HAND (POTENTIAL)
FT	SEQUENCE 423 AA; 46306 MW; 67CAAC76DA531A71 CRC64;
Query Match	16.5%; Score 333; DB 1; Length 423;
Best Local Similarity	25.3%; Pred. No. 1.le-16;
Matches 118; Conservative	%63; Mismatches 130; Indels 92; Gaps 19;
QY	51 LPPAS-SGDSG-----SLATSIQMVKTEKGAKRKTSSEKNGSSEL---- 92
Db	34 LPSSCGDGMKDSSFEINTRODSLTSSSAVAGVD-----ISAGEINSGDEFPFRS 87
QY	93 ---VEKKVCK--ASSVFGLKY-----VAERKGEREEMOD-----ARVLIND 130 : :
Db	88 MNQSEKKVLSRTESRSLEFKCVPLGYVTSCGRPEMEDSVSTIPRFIQVSSSSLLDGR 147 : :
QY	131 ITECRPPSSLITRVSVFVFDGHGGIRASKFAQNHL-----ONLIRPKP---GDVISV 183 : : : : : :
Db	148 VTNGFNPHLS-----AHFFGVYDGHGSQVAN YCRRMHIALTEEIVKEKPFCFGD--TW 201 : : : : :
QY	184 EKVTKRCILDTFKHTDEEFLQASSQKPAWKOGSTATCVLADNTLYLTANIGDSRAILCR 243 : : : : : : :
Db	202 QEKWKQALFNFMVRWDSEIETVAHAPETV---GSTSVVAVPFPPTHIFVANGDSRAVLUR 259 : : : : : :
QY	244 YNESSQHAALSLSKEHNPTQYEERMRIQKAGNV---RDGRVLGVLEYSRISIDGQYKR 300 : : : : : : :
Db	259 -----GKTPLALSVDHKHPDDDEARIENAAEGKVIWNVGARVFGVLAMSRISGD-RYLK 311 : : : : : : :
QY	301 CGVTSVPDIRSQTPPNDRPELLACDGLFKVFTPEEAVNF-----IL-----SCL 345 : : : : : : :
Db	312 PSVIPDPETVSRRVKEDDCILLASDGLMDWMTNEEVCDLARKRILLHEKKNAMAGEALL 371 : : : : : : :
QY	346 EDEKIQTREGKSADARYEAACHNRLANKA VQRGSAQNTVMVV 388 : : : : : : :
Db	372 PAEK--RGEGK---DPAAMGAAYELSKVALQKSGKONI SVVVV 409 : : : : : : :

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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; D17411; BAA04233.1; -
DR	EMBL; D17412; BAA04234.1; -
DR	EMBL; D45859; BAA08293.1; -
DR	EMBL; D45860; BAA08294.1; -
DR	EMBL; D45861; BAA08295.1; -
DR	EMBL; U09218; AAB60442.1; -
DR	EMBL; AB007798; BAA84471.1; -
DR	EMBL; AB007794; BAA84471.1; JOINED.
DR	EMBL; AB007795; BAA84471.1; JOINED.
DR	EMBL; AB007796; BAA84471.1; JOINED.
DR	EMBL; AB007797; BAA84471.1; JOINED.
DR	PIR; I49016; I49016.
DR	PIR; S65672; S65672.
DR	HSP; P35813; I4GQ.
DR	MGI; MGI:101841; Pgm1b.
DR	InterPro; IPR001932; PP2C-like.
DR	InterPro; IPR000222; PF2C.
DR	Pfam; PF00481; PP2C; 1.
DR	SMART; SM00331; PP2C SIG; 1.
DR	SMART; SM00332; PP2CG; 1.
DR	PROSITE; PS01032; PP2C; 1.
DR	Hydrolase; Magnesium; Manganese; Multigene family;
KW	Hydrolyase; Magnesium; Manganese; Multigene family;

[illegible]

Qy 303 -VTSVPDIRCQLTNPDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKGAADA 361
Db 219 LVSPEPEVYELLRAEDEFVVLACDGIWDVMSNEELCEFNRL-----VSD 266
Qy 362 RYEAACNRLANKAVORGSDNVTVMV 388
Db 267 DLENVCNWWDTCLHKGSRDNNMSIVLV 293

Search completed: April 12, 2004, 09:06:41
Job time : 18 secs

OM protein - protein search, using sw model

Run on: April 12, 2004, 09:03:32 ; Search time 45 Seconds
(without alignments)
2748.514 Million cell updates/sec

Title: US-09-935-124A-2

Perfect score: 2018
Sequence: 1 MDLFGDLPEPRSPRAAGK.....KAVQGSADNVTVVVRIGH 392

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2018	100.0	392	4	Q9H0C8 homo sapien
2	1935	95.9	392	11	Q8R0F6
3	1931	95.7	392	11	Q9Z1Z6
4	1078	53.4	212	11	Q9CG46
5	856	42.4	167	11	Q9Z0T2
6	728	36.1	385	5	Q86F00
7	481	23.8	341	10	Q9LMT1
8	480	23.8	351	10	Q944X0
9	474	23.5	242	5	O62212
10	408.5	20.2	319	10	Q8S8Z0
11	398.5	19.7	311	10	Q8RXV3
12	391	19.4	282	10	Q7XR05
13	381.5	18.9	243	10	Q8S3P1
14	370.5	18.4	354	10	Q8LAY8
15	368.5	18.3	420	10	Q8VZD9
16	368	18.2	319	5	Q7YUT1

17	368	18.2	389	10	O81773
18	368	18.2	975	5	O15743
19	366.5	18.2	420	10	Q94AT1
20	366.5	18.2	757	4	Q9UPT0
21	365	18.1	359	10	O82469
22	365	18.1	766	4	Q8WY54
23	364.5	18.1	348	10	Q9LEW5
24	364.5	18.1	371	10	Q8VZN9
25	362	17.9	464	10	Q9FXE4
26	361	17.9	380	10	Q8RX37
27	361	17.9	750	11	Q80Z30
28	359.5	17.8	388	10	Q8H610
29	358.5	17.8	361	10	Q9SD02
30	358.5	17.8	665	11	Q80T10
31	356	17.6	643	11	Q8CB81
32	353.5	17.5	355	10	O81716
33	353.5	17.5	362	10	Q9ZPL9
34	353.5	17.5	438	3	Q7Z8P2
35	352	17.4	307	10	Q9FGM3
36	352	17.4	392	10	Q9SLA1
37	351	17.4	404	10	O22200
38	351	17.4	658	10	Q940A2
39	350	17.3	305	10	Q942N4
40	350	17.3	357	10	Q9S253
41	342	16.9	439	3	Q872D8
42	340	16.8	1148	5	Q86A16
43	339	16.8	396	10	Q9LP12
44	338.5	16.8	383	10	Q9MLP8
45	338.5	16.8	390	10	Q9XEE8

ALIGNMENTS

RESULT 1

Q9H0C8	PRELIMINARY;	PRT;	392 AA.
ID	Q9H0C8		
AC	Q9H0C8		
DT	01-MAR-2001 (TRENBLrel. 16, Created)		
DT	01-MAR-2001 (TRENBLrel. 16, Last sequence update)		
DT	01-OCT-2003 (TRENBLrel. 25, Last annotation update)		
DE	Hypothetical protein (Integrin-linked kinase-associated serine/threonine phosphatase 2C).		
DE	serine/threonine phosphatase 2C).		
GN	DKE2P34J2031		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Testis;		
RA	Blum H., Bauersachs S., Mewes H.W., Weil B., Wiemann S.;		
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Leung-Hageteijn C., Mahendra A., Naruszewicz I., Hannigan G.E.;		
RT	"Modulation of integrin signal transduction by ILKAP, a protein phosphatase 2C associating with the integrin-linked kinase, ILK1."		
RL	EMBO J. 0:0-0(2001).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Uterus;		
RA	Straussberg R.;		
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.		
CC	- 1- SIMILARITY: BELONGS TO THE PP2C FAMILY.		
DR	EMBL; AL136850; CAB66784.1; -		
DR	EMBL; AY024365; AAK07736.1; -		
DR	EMBL; BC008576; AAH06576.1; -		
DR	HSSP; P35813; 1A6Q.		
DR	Genew; HGNC:15566; ILKAP.		
DR	GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.		
DR	GO; GO:0016781; F:hydrolase activity; IEA.		
DR	GO; GO:0016301; F:kinase activity; IEA.		

DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hypothetical protein; Hydrolase; Kinase; Magnesium.
SQ SEQUENCE 392 AA; 42906 MW; AF6ACC98508CBEA3 CRC64;

Query Match 100.0%; Score 2018; DB 4; Length 392;
Best Local Similarity 100.0%; Pred. No. 5.8e-154;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPRAAGKAQKGLLFDLPPASSTDSGGPGLLFDLPPASSGDSG 60
DB 1 MDLFGDLPEPERSPPRAAGKAQKGLLFDLPPASSTDSGGPGLLFDLPPASSGDSG 60
QY 61 SLATSIQWVTEGKAGKKTSEEEKNGSEBELVEKKVKCASSVIFGLKGYVAERKGEREE 120
DB 61 SLATSIQWVTEGKAGKKTSEEEKNGSEBELVEKKVKCASSVIFGLKGYVAERKGEREE 120
QY 121 MQDAHVLNDITEECRPPSSLIIRVSYFAVFDGHHGIRASKFAAQNHLNLRKPKGDV 180
DB 121 MQDAHVLNDITEECRPPSSLIIRVSYFAVFDGHHGIRASKFAAQNHLNLRKPKGDV 180
QY 181 ISVEKTVKRCCLDTPFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLGDRAI 240
DB 181 ISVEKTVKRCCLDTPFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLGDRAI 240
QY 241 LCRYNEESQKHAALSLSKEHNPTQYEERMRICKAGNVDRGVLGVLEVSRSIGDQYKR 300
DB 241 LCRYNEESQKHAALSLSKEHNPTQYEERMRICKAGNVDRGVLGVLEVSRSIGDQYKR 300
QY 301 CGVTSVPDIRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
DB 301 CGVTSVPDIRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
QY 361 ARYEACNRLANKAVQGSADNVTVVVRIGH 392
DB 361 ARYEACNRLANKAVQGSADNVTVVVRIGH 392

RESULT 2
Q8R0F6 PRELIMINARY; PRT; 392 AA.
AC Q8R0F6
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to protein phosphatase 2C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
DR EMBL; BC026953; AAH26953.1; -.
DR GO; GO:0000287; F:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.

DR SMART; SM00331; PP2C SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydrolase; Magnesium.
SQ SEQUENCE 392 AA; 42774 MW; 8DE1F77DAC9B7176 CRC64;

Query Match 95.9%; Score 1935; DB 11; Length 392;
Best Local Similarity 95.2%; Pred. No. 2.7e-147;
Matches 373; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPRAAGKAQKGLLFDLPPASSTDSGGPGLLFDLPPASSGDSG 60
DB 1 MDLFGDLPEPERSPPRAAGKAQKGLLFDLPPASSTDSGGPGLLFDLPPASSGDSG 60
QY 61 SLATSIQWVTEGKAGKKTSEEEKNGSEBELVEKKVKCASSVIFGLKGYVAERKGEREE 120
DB 61 SLATSIQWVTEGKAGKKTSEEEKNGSEBELVEKKVKCASSVIFGLKGYVAERKGEREE 120
QY 121 MQDAHVLNDITEECRPPSSLIIRVSYFAVFDGHHGIRASKFAAQNHLNLRKPKGDV 180
DB 121 MQDAHVLNDITEECRPPSSLIIRVSYFAVFDGHHGIRASKFAAQNHLNLRKPKGDV 180
QY 181 ISVEKTVKRCCLDTPFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLGDRAI 240
DB 181 ISVEKTVKRCCLDTPFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLGDRAI 240
QY 241 LCRYNEESQKHAALSLSKEHNPTQYEERMRICKAGNVDRGVLGVLEVSRSIGDQYKR 300
DB 241 LCRYNEESQKHAALSLSKEHNPTQYEERMRICKAGNVDRGVLGVLEVSRSIGDQYKR 300
QY 301 CGVTSVPDIRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
DB 301 CGVTSVPDIRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
QY 361 ARYEACNRLANKAVQGSADNVTVVVRIGH 392
DB 361 ARYEACNRLANKAVQGSADNVTVVVRIGH 392

RESULT 3
Q9Z1Z6 PRELIMINARY; PRT; 392 AA.
AC Q9Z1Z6
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Protein phosphatase 2C.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99074314; PubMed=9857069;
RA Tong Y., Quirion R., Shen S.H.;
RT "Cloning and characterization of a novel mammalian PP2C isozyme."
RL J. Biol. Chem. 273:35282-35290(1998).
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
DR EMBL; AF095927; AAC97497.1; -.
DR HSSP; P35813; 1A6Q.
DR GO; GO:0000287; F:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydrolase; Magnesium.
SQ SEQUENCE 392 AA; 42744 MW; 1468FDE0BA60D915 CRC64;

Query Match 95.7%; Score 1931; DB 11; Length 392;
Best Local Similarity 95.4%; Pred. No. 5.8e-147;
Matches 373; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERPRPAAGKEAQKGLLFDLPPASSTDSGGPFLFDLPPASSGDSG 60
DB 1 MDLFGDLPEPERPRPSAGKEAQEGVLPEDLPPTSTDSGGPFLFDLPPAGNSG 60

QY 61 SLATISQWVKTGKAGKRTSEENKNGSEELVEKKVCKASSVIFGLKYGVAKRGERE 120
DB 61 SLATSGQVVKNEGKAGKAPKEENKNGSEELVEKKVCKASSVIFGLKYGVAKRGERE 120

QY 121 MQDAHVLNDITRECPSPSLITRVSYFAVFDGHHGIRASKPAQNLHQLIRKPKGDV 180
DB 121 MQDAHVLNDITRECPSPSLITRVSYFAVFDGHHGIRASKPAQNLHQLIRKPKGDV 180

QY 181 ISVEKTVKRCCLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDRAI 240
DB 181 ISVEKTVKRCCLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDRAI 240

QY 241 LCRYNESQKHAALSLSKEHNPTQYERMRIOKAGNVDRGVLGVLEVSRSIGDQYKR 300
DB 241 LCRYNESQKHAALSLSKEHNPTQYERMRIOKAGNVDRGVLGVLEVSRSIGDQYKR 300

QY 301 CGVTSVPDIRCOLTPNDRIILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
DB 301 CGVTSVPDIRCOLTPNDRIILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360

QY 361 ARYEACNRLANKAVORGSDADNTVMVVRIGH 392
DB 361 ARYEACNRLANKAVORGSDADNTVMVVRIGH 392

RESULT 4
Q9CS46 PRELIMINARY; PRT; 212 AA.

ID Q9CS46 AC Q9CS46; TISSUE=Embryo;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 0710007A14RIK protein (Fragment).
GN 0710007A14RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21095660; PubMed=11217851;
RA Kawai J., Shinesawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staehli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyrshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK019158; BAB31574.1; -.
DR HSSP; P35813; 1A6Q
DR MGD; MGI:1914694; 0710007A14RIK.

GO: GO:0003824; F: catalytic activity; IEA.
InterPro; IPR001932; P2C-Like.
PFam; PF00481; P2C; 1.
DR SMART; SM00332; P2C; 1.
FT NON TER 1
SQ SEQUENCE 212 AA; 23615 MW; 133286D628B540D7 CRC64;

Query Match 53.4%; Score 1078; DB 11; Length 212;
Best Local Similarity 98.1%; Pred. No. 9.8e-79;
Matches 208; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 181 ISVEKTVKRCCLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDRAI 240
DB 1 ISVEKTVKRCCLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDRAI 240

QY 241 LCRYNESQKHAALSLSKEHNPTQYERMRIOKAGNVDRGVLGVLEVSRSIGDQYKR 300
DB 61 LCRYNESQKHAALSLSKEHNPTQYERMRIOKAGNVDRGVLGVLEVSRSIGDQYKR 120

QY 301 CGVTSVPDIRCOLTPNDRIILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
DB 121 CGVTSVPDIRCOLTPNDRIILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360

QY 361 ARYEACNRLANKAVORGSDADNTVMVVRIGH 392
DB 181 ARYEACNRLANKAVORGSDADNTVMVVRIGH 212

RESULT 5
Q9Z0T2 PRELIMINARY; PRT; 167 AA.

ID Q9Z0T2 AC Q9Z0T2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
GN 0710007A14RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Stothard P.M., Pilgrim D.;
RT "Isolation of P2C sequences using degenerate-oligo PCR."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF117831; AAD17234.1; -.
DR HSSP; P35813; 1A6Q.
DR MGD; MGI:1914694; 0710007A14RIK.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR InterPro; IPR001932; P2C-Like.
DR PFam; PF00481; P2C; 1.
DR SMART; SM00332; P2C; 1.
KW Hypothetical protein.
FT NON TER 1
FT NON TER 167
SQ SEQUENCE 167 AA; 18795 MW; 3A4FC2EFB09D95B CRC64;

Query Match 42.4%; Score 856; DB 11; Length 167;
Best Local Similarity 98.8%; Pred. No. 5e-61;
Matches 165; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 157 IRASKFAAQNLHQLIRKPKGDVISEKTVKRCCLDTFKHTDEEFLKQASSQKPAWKD 216
DB 1 IRASKFAAQNLHQLIRKPKGDVISEKTVKRCCLDTFKHTDEEFLKQASSQKPAWKD 60

QY 217 STATCVLAVDNILYIANLGDRAILCRYNESQKHAALSLSKEHNPTQYERMRIOKAG 276
DB 61 STATCVLAVDNILYIANLGDRAILCRYNESQKHAALSLSKEHNPTQYERMRIOKAG 120

QY 277 NVDRGVLGVLEVSRSIGDQYKCGVTSVPDIRCOLTPNDRIILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 323

Db 121 NVDRGVLVGVLEVSRSIGGGYKRCGVTSVPDIRRCQLTPNDRFILL 167

RESULT 6

Q86F00 PRELIMINARY; PRT; 385 AA.

ID Q86F00

AC Q86F00

DT 01-JUN-2003 (Tremblrel. 24, Created)

DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Clone ZD21250 mRNA sequence.

OS Schistosoma japonicum (Blood fluke).

OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidida;

OC Schistosomatidae; Schistosomatidae; Schistosoma.

OX NCBI_TaxID=6182;

RN [1]

RP SEQUENCE FROM N.A.

RA Liu F., Hu W., Yan Q., Xu X., Zhu Z., Zhang X., Wang J., Sun J.,

RA Xu X., Wang Z., Zeng L., Rong Y., Wu X., Qu J., Xu Z., Huang J.,

RA Ma Y., Wang S., Wang Z., Xue C., Feng Z., Chen Z., Han Z.,

RT "The full-length cDNA of S. japonicum genes."

RL Submitted (JAN-2003) to the EMBL/GenBank/DBSJ databases.

DR EMBL: AY223064; AAP06087.1; -.

DR GO: GO:0008287; C:protein serine/threonine phosphatase complex; IEA.

DR GO: GO:0003824; F:catalytic activity; IEA.

DR GO: GO:0004722; F:protein serine/threonine phosphatase activity; IEA.

DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.

DR InterPro: IPR000222; PP2C.

DR InterPro: IPR001932; PP2C-like.

DR Pfam: PF00481; PP2C; 1.

DR SMART: SM00332; PP2C; 1.

DR PROSITE: PS01032; PP2C; 1.

SQ SEQUENCE 385 AA; 43372 MW; 74D60E17D11073EE CRC64;

Query Match 36.1%; Score 728; DB 5; Length 385;

Best Local Similarity 40.3%; Pred. No. 3.3e-50;

Matches 153; Conservative 62; Mismatches 91; Indels 74; Gaps 6;

QY 47 LPDDLPPASSGDSGLATSIQWKTGKAKRTSEEEKNGSEELVEKK----- 96

Db 3 LPDDLPEPS-----VESDEIQKSETLIEDSSWNEPESVSK 37

QY 97 ---VCKASSVIFGLKGVVAERKGERBERMDAHVLNDITEC-RPSSLLITRVSFAVF 151

Db 38 ITPFTCS-----VARKGERPEMQDSHVIVNDLADSMRPGVSEILRVCYFAVF 86

QY 152 DGHGIRASKFAAQNHLNLRKPKGDVIVSEKTKRCLLDTFKHTDEBFLKQASSQKP 211

Db 87 DGHGAKAANFACKELHDIARPRGGIQOQVEKDKKVLVDSYKTTDEBFLRACQRP 146

QY 212 AWKDGSTATCVLAVNLIYANLGDRAILCRYNE-----ESQKHAALS 255

Db 147 HWRDGSTAATILLVNDTLTYIGNLGDVKVLLARVLESLSSESNPNVNGNILLSKLSAIC 206

QY 256 LSKEHNPTQYERMRIOKAGNVRDGRVLGVLEVSRSIGDQYKRCGVTSVPDIRRCQLT 315

Db 207 LTKDENPDYERQRIQATGASVQNGRVSLEVSRSFGDYQPKQGVTCIPDVRKCOLT 266

QY 316 PNDRILLACDGLPKVTPPEAVNFILSCL-----EDEKIQTRREGKSAADARYEAACN 368

Db 267 QNDQFLLACDGLKWSFPDPAVHLTHRLMQEIKNHENQKSNQDQIFQCRHLDVSVA 326

QY 369 RLANKAVQSGADNVTVMVV 388

Db 327 HLIVNEAVLRMSGDNVTCILL 346

RESULT 7

Q9LMT1 PRELIMINARY; PRT; 341 AA.

ID Q9LMT1

AC Q9LMT1

DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

Db 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE At1g18030/T10F20.3.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OX eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Sakano H., Liu S.X., Etgu P., Lee J.M., Lenz C., Pham P., Toriumi M.,

RA Yu G., Chan A., Chung M., Goldsmith A., Liu A., Smith A., Vaysberg M.,

RA Altati H., Brooks S., Buehler B., Chao Q., Conn L., Conway A.B.,

RA Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M.,

RA Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R.,

RA Pederspiel N.A., Theologis A.

RT "The sequence of BAC T10F20 from Arabidopsis thaliana chromosome 1."

RL Submitted (AUG-2000) to the EMBL/GenBank/DBSJ databases.

DR EMBL: AC034107; AAF97840.1; -.

DR PIR: G86315; G86315.

DR HSSP: P35813; 1A60.

DR GO: GO:0003824; F:catalytic activity; IEA.

DR InterPro: IPR001932; PP2C-like.

DR Pfam: PF00481; PP2C; 1.

DR SMART: SM00332; PP2C; 1.

DR SMART: SM00331; PP2C SIG; 1.

SQ SEQUENCE 341 AA; 37367 MW; 6873C0CE82310195 CRC64;

Query Match 23.8%; Score 481; DB 10; Length 341;

Best Local Similarity 35.8%; Pred. No. 2e-30;

Matches 119; Conservative 66; Mismatches 107; Indels 40; Gaps 11;

QY 78 KBKTSEEEKNGSEELV-----EKKYCKASSVI-----FGLKGVVAERKGERBERMDAHVI 127

Db 24 KAKKSEVSGGGEAAVAGNREAEEDKPSFVSEKKEFLVEADVAEDKGRARTMEDVWVV 83

QY 128 LNDITEECRPSLLITRVSFAVFEDHGIGIRASKFAAQNHLNLRKPKGDVIVSEKTV 187

Db 84 LPDASLDF--PQTL--RCAHFAIYDGHGRLAAEFKXHLHUNLVISAGLPRELLDV-KVA 138

QY 188 KRCLLDTFKHTDEEFLKQASSQKPAWKDGSTATCVLAVNLIYANLGDRAILCR---- 243

Db 139 KKAILEGFKTDELLLOKQSV--GGQDGAATVAVCWILDQKVFVANIGDAKAVLARSTT 196

QY 244 -----YNESQKHAALSLSKEHNPTQYERMRIOKAGNV-RDGRVLGVLEVSRSIGDQ 297

Db 197 NELGNHTEAGNPLKAILVTRHKAIYQPSRSIQKSGGVISSNGRLQGRLEYSRAFGRH 256

QY 298 YRCGVTSVPDIRRCQLTPNDRFILLACDGLPKVTPPEAVNFILSCLDEKIQTRREGK 357

Db 257 FKFGVSAFTDIAFELTERENFMILGCDGLWEVFGPSDAVGFQKLL-----KEG-- 307

QY 358 AADARYEAAACNRLANKAV-ORGSADNVTVMVV 388

Db 308 ----LHVSTVSRRLVKEAVKERRCKNCTAIVI 336

RESULT 8

Q944K0 PRELIMINARY; PRT; 351 AA.

ID Q944K0

AC Q944K0

DT 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE At1g18030/T10F20.3.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OX eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kaniya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.,
RT "Arabidopsis cDNA clones";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF428352; AAL16282.1; -
DR GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2CC; 1.
DR SMART; SM00331; PP2C SIG; 1.
SQ SEQUENCE 351 AA; 38514 MW; AFE224E0EE003229 CRC64;
Query Match 23.8%; Score 480; DB 10; Length 351;
Best Local Similarity 35.8%; Pred. No. 2.5e-10;
Matches 119; Conservative 66; Mismatches 107; Indels 40; Gaps 11;
QY 78 KRKTSSEKNGSELV-----EKVKCKASSVI-----FGLKGVYAEKGEREEMQDAHYI 127
DB 34 KAKKSEVSGGGAAGVAGNREVEEKPFSVSEKKEFLVEADVAEDKARHTMEDVWV 93
QY 128 LNDITECRPSSLIITRVSYFAVFDGHHGIRASKFAAQNLHQLNLRKPKGDVISVEKTV 187
DB 94 LPDASLDF--PGTL--RCAHFAIYDGGHGLAAEFKAKHLNVLGSLPRELLDV-KVA 148
QY 188 KRCLDTFKTDEFLKQASSQKPAWKGSTATCVLAVDNLILYIANLGSRAILCR---- 243
DB 149 KKAILEGFRKTDLELLQKSVS--GGWDGATATVCMVILDKQVFNIGDAKAVLARSTT 206
QY 244 -----YNEESQKHAALSLSKEHNPTQYERMRIOKAGNV-RDGRVLGVLEYSRSIGDQ 297
DB 207 NELGNTEAGNPKAIVLTREHKAIVPQERSIRQKSGGVSSNGRLQGRLEVSRAFGDRH 266
QY 298 YKCGVTSPDIRRCOLTPNDRIILLACGLFKVFTPEEAVNFIILSCLEDEKIQTRGKS 357
DB 267 FKFGVSATDIIHAFELTERENFMILCCDLNLFVFGPSDAVGQKLL-----KEG-- 317
QY 358 AADARYEACNRLANKAV-ORGSDNVTVMV 388
DB 318 --LHVTSTVSRLLVKEAVKERRCKNDCTAIVI 346
RESULT 9
ID O62212 PRELIMINARY; PRT; 242 AA.
AC O62212;
DT 01-AUG-1998 (TremBLrel. 07, Created)
DT 01-NOV-1998 (TremBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE F33A8.6 protein.
GN F33A8.6
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,

RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA Smdalson N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans";
RL Nature 368:32-38 (1994).
RN [3]
RP SEQUENCE FROM N.A.
RA Mortimore B.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
DR EMBL; Z81525; CAB04260.1; -
DR EMBL; AL031284; CAB04260.1; JOINED.
DR EMBL; AL031264; CAA20326.1; -
DR EMBL; Z81525; CAA20326.1; JOINED.
DR PIR; T18588; T18588.
DR WormPep; F33A8.6; C818659.
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0036787; F:hydrolase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2CC; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydrolase; Magnesium.
SQ SEQUENCE 242 AA; 26845 MW; 62B6CA6104D34ADC CRC64;
Query Match 23.5%; Score 474; DB 5; Length 242;
Best Local Similarity 40.2%; Pred. No. 4.6e-30;
Matches 98; Conservative 54; Mismatches 80; Indels 12; Gaps 5;
QY 82 SEEEKNGSELV-----EKVKCKASSVIFGLKGVYAEKGEREEMQDAHYI--DITEEC 135
DB 3 SDSRKRSDDLLDSDSKPKESRNLTYTAAVCGKRGADWDTHIMLPKFDLGTGTE- 61
QY 136 RPPSLITRVSYFAVFDGHHGIRASKFAAQNLHQLNLRKPK-GDVISVEKTVKRLDIT 194
DB 62 --KSFISRASFAIFDGHAGPRAEHQCSQMGKTVKEKLAKFSDFFTLTSLKQTETES 118
QY 195 FKHTDEEFLKQASSQKPAWKGSTATCVLAVDNLILYIANLGSRAILCRVNEESQKHAAL 254
DB 119 YKAVDDGFLATAKQNKPIKDGTTATTMIILANNVIYVANIGDSRAVVARKEKG-SFAPV 177
QY 255 SLSKEHNPTQYERMRIOKAGNVDRGVLEVSRSIGDQVKRCGVTSVPDIRCQL 314
DB 178 CLTVDHDPMSHDERMRIOKAGAVVKGDRINGVIEVSRSIGDLPFKSLGIISTPDLKKLTL 237
QY 315 TPND 318
DB 238 TKND 241
RESULT 10
ID Q888Z0 PRELIMINARY; PRT; 319 AA.
AC Q888Z0;
DT 01-JUN-2002 (TremBLrel. 21, Created)
DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Protein phosphatase 2C.
GN MPC9.
OS Mesembryanthemum crystallinum (Common ice plant).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Alzooceae; Mesembryanthemum.
OX NCBI_TaxID=3544;
RN [1]
RP SEQUENCE FROM N.A.
RA Miyazaki S., Izumi S., Fukuhara T., Bohnert H.J.;

"Plant Protein Phosphatases 2C ? A large protein family serving complex functions." ;

RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.

DR EMBL; AB083482; BAB8944.1; -

DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.

DR GO; GO:0016787; F:hydrolase activity; IEA.

DR GO; GO:0000287; F:magnesium ion binding; IEA.

DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.

DR GO; GO:0006470; F:protein amino acid dephosphorylation; IEA.

DR InterPro; IPR000222; PP2C.

DR InterPro; IPR001932; PP2C-like.

DR Pfam; PF00481; PP2C; 1.

DR SMART; SM00332; PP2C; 1.

DR SMART; SM00331; PP2C_S1G; 1.

DR PROSITE; PS01032; PP2C; 1.

KW Hydrolase; Magnesium.

SQ SEQUENCE 319 AA; 34477 MW; 0BD228603E34CFB0 CRC64;

Query Match 20.2%; Score 408.5; DB 10; Length 319;

Best Local Similarity 39.6%; Pred. No. 1.3e-24;

Matches 113; Conservative 41; Mismatches 86; Indels 45; Gaps 12;

QY 109 GYVAERKGEREMQDAHVILNDITECRPPSLITRVSYFAVFDGHHGIRASKFAAQNLH 168

DB 35 GY-ASSPKRSSMEDFYETRIDVVG-----EVGLFGVFDGHHGIRAAEYVKQNLF 85

QY 169 QNLIRKFKGDVISVEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKD-GSTATCVLAVDN 227

DB 86 SNLI-KHPK--FIS--DTKSAIAEAYTHTDSEFLKSENTQN--RDAGSTASTAILVGD 136

QY 228 ILVIANLGDRAILCRYNESQKHAALSKEHNPTQYEEHMRICKAGNVR---DGRVL 284

DB 137 RLLVANVGDSRAVICRGGE-----AIAVSRDHKPDQSDERQIEDAGGFVMAWGTWRVG 190

QY 285 GYLVSRISGDQYKRCGVTSVPDIRRCOLTNDREIFILLACDGLFKVFPPEAVNFILSC 344

DB 191 GYLVASRAFGDKLLKQY-VVADPEIQEEVDSLEFLILASDGLMDVNVNEAVTMV--- 246

QY 345 LEDEKIQTRGKSAADARYEAACNLANKAVORGSDNVTVMVVR 389

DB 247 -----KPIQDT--EEAKLMQEAYQSGADNITCVVR 278

RESULT 11

Q8RXV3 PRELIMINARY; PRT; 311 AA.

AC Q8RXV3; 21, Created

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.

GN Ar4G31750.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCB_TaxID=3702;

[1]

SEQUENCE FROM N.A.

RA Yamaoka K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Miramanda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.

RT "Arabidopsis Full Length cDNA Clones."

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.

RA Yamaoka K., Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hsuan V.W., Lee J.M., Quach H.L., Tang C., Toriumi M., Wu H.C., Yu G., Bowser L.,

RA Carninci P., Chen H., Cheuk R., Hayaishizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Miramanda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.

RT "Arabidopsis Open Reading Frame (ORF) Clones."

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.

DR EMBL; AY080658; AAL86334.1; -

DR EMBL; AY133761; AM91695.1; -

DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.

DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.

DR GO; GO:0005488; F:binding; IEA.

DR GO; GO:0016787; F:hydrolase activity; IEA.

DR GO; GO:0000287; F:magnesium ion binding; IEA.

DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.

DR GO; GO:0006470; F:protein amino acid dephosphorylation; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR001993; Mitoch_carrier.

DR InterPro; IPR000222; PP2C.

DR InterPro; IPR001932; PP2C-like.

DR Pfam; PF00481; PP2C; 1.

DR PROSITE; PS00215; MITOCH_CARRIER; 1.

DR PROSITE; PS01032; PP2C; 1.

KW Hypothetical protein; Hydrolase; Magnesium.

SQ SEQUENCE 311 AA; 33247 MW; 5E3098B91F116BFD CRC64;

Query Match 19.7%; Score 398.5; DB 10; Length 311;

Best Local Similarity 39.3%; Pred. No. 7.7e-24;

Matches 112; Conservative 40; Mismatches 88; Indels 45; Gaps 12;

QY 109 GYVAERKGEREMQDAHVILNDITECRPPSLITRVSYFAVFDGHHGIRASKFAAQNLH 168

DB 35 GY-ASSPKRSSMEDFYETRIDVVG-----EVGLFGVFDGHHGIRAAEYVKQNLF 85

QY 169 QNLIRKFKGDVISVEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKD-GSTATCVLAVDN 227

DB 86 SNLI-RHPK--FIS--DTTAAADAYNTDSEFLKSENSQN--RDAGSTASTAILVGD 136

QY 228 ILVIANLGDRAILCRYNESQKHAALSKEHNPTQYEEHMRICKAGNVR---DGRVL 284

DB 137 RLLVANVGDSRAVICRGGN-----AIAVSRDHKPDQSDERQIEDAGGFVMAWGTWRVG 190

QY 285 GYLVSRISGDQYKRCGVTSVPDIRRCOLTNDREIFILLACDGLFKVFPPEAVNFILSC 344

DB 191 GYLVASRAFGDKLLKQY-VVADPEIQEEKVSLEFLILASDGLMDVNVNEAVGMI-KA 248

QY 345 LEDEKIQTRGKSAADARYEAACNLANKAVORGSDNVTVMVVR 389

DB 249 IEDP-----EAGKRLMEAYQSGADNITCVVR 278

RESULT 12

Q7XR05 PRELIMINARY; PRT; 282 AA.

AC Q7XR05; 25, Created

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE OSUNBA0015K02.8 protein.

GN OSUNBA0015K02.8.

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzoideae; Oryza.

OX NCB_TaxID=4530;

[1]

SEQUENCE FROM N.A.

RA Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X., Qian Y.W., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,

RA Ren S.X., Lv G., Lin W., Gu W.O., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,
RA Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun X.,
RA Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
RA Gu J.L., Chen S.T., Xi L., Zhu F.H., Hong G.F.,
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL606608; CA02891.1; -
SQ SEQUENCE 282 AA; 30584 MW; B8FF3CF119534AB7 CRC64;
Query Match 19.4%; Score 391; DB 10; Length 282;
Best Local Similarity 36.7%; Pred. No. 2.7e-23;
Matches 106; Conservative 46; Mismatches 89; Indels 48; Gaps 9;
QY 109 GYVAERKGREREMQDAHVILNDITECRPPSSLIITRVSYFAVFDGHHGIRASKFAAQNLIH 168
DB 29 GY-ASPGKASWDFY-----ETRIDSDVGQIIGLFGVFDGHHGAKVAEYVKQNL 79
QY 169 ONLIR--KPPKGDVISEVKTAKRCLLDTFKITDEEFLKQASSQKPAWKDGSTATCVLAVD 226
DB 80 SHLLRHPKFISTDVAID-----DAYKSTDSFLESDSSQNC---GSTASTAVLVG 128
QY 227 NLYLTANLGDRAILCRNEESQKHAALSKEHNPTQYERMIQKAGNVR---DGRV 283
DB 129 DSLFVAVNGDSRAIICRGNG-----AIAVSKDHKPKDQTDQRIEDAGGFVMMAGTWRV 182
QY 284 LGVLEVSIGDQVKRCQVTSVPDIRCQLTNDREFILLACDGLFKVFTPEEAVNFILS 343
DB 183 GGVLAVSRAFGDKLKQYVVD--PEIREVIDHSELEFILLASDGLDWDVVTNEEAVDMTRS 241
QY 344 CLEDEKIQITREKSAADARYEAACNRLANKAVQSGADNVTVMVVRICH 392
DB 242 IHPDEE-----AAKLLQEAQYKRESSDNTICVVVRFLH 274
RESULT 13
Q8S3P1 PRELIMINARY; PRT; 243 AA.
AC Q8S3P1
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DE Hypothetical protein.
GN 24K23.16.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Park Y.-J., Rostoks N., Ramakrishna W., SanMiguel P., Shiloff B.,
RA Ma J., Jiang Z., Kleinbols A., Bennetzen J.;
RT "Sequence characterization of orthologous regions in the barley and
RT rice genomes."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE PF2C FAMILY.
DR EMBL; AF480497; AAL87187.1; -
DR Gramene; Q8S3P1; -
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR000222; P2PC.
DR InterPro; IPR001932; P2PC-like.
DR Pfam; PF00481; P2PC; 1.
DR SMART; SM00332; P2PC; 1.
DR SMART; SM00331; P2PC SIG; 1.
DR PROSITE; PS00215; MITOCH_CARRIER; 1.

DR PROSITE; PS01032; PP2C; 1.
KW Hypothetical protein; Hydrolase; Magnesium.
SQ SEQUENCE 243 AA; 26734 MW; B8481E17F559CE5F CRC64;
Query Match 18.9%; Score 381.5; DB 10; Length 243;
Best Local Similarity 37.9%; Pred. No. 1.3e-22;
Matches 96; Conservative 43; Mismatches 75; Indels 39; Gaps 7;
QY 145 VSYFAVFDGHHGIRASKFAAQNLIHQLIR--KPPKGDVISEVKTAKRCLLDTFKHTDEEF 202
DB 17 IGLFGVFDGHHGAKVAEYVKQNLFSHLLRHPKFISTDVAID-----DAYKSTDSF 68
QY 203 LKQASSQKPAWKDGSTATCVLAVDNILYIANLGDRAILCRNEESQKHAALSKEHNP 262
DB 69 LESDSSQNC---GSTASTAVLVGDRLFVAVNGDSRAIICRGNG-----AIAVSKDHK 119
QY 263 TQYERMIQKAGNVR---DGRVLEVSRSIGDQVKRCQVTSVPDIRCQLTNDREFILLACDGLFKVFTPEEAVNFILS 379
DB 120 DQTDQRIEDAGGFVMMAGTWRVGGVLAVSRAFGDKLKQYVVD--PEIREVIDHSE 178
QY 320 FILLACDGLFKVFTPEEAVNFILSCLDEKIQITREKSAADARYEAACNRLANKAVQSGS 379
DB 179 FILLASDGLDWDVVTNEEAVDMTRSIDHDEE-----AAKLLQEAQYKRES 222
QY 380 ADNVTVMVVRICH 392
DB 223 SDNITCVVVRFLH 235
RESULT 14
Q8LAY8 PRELIMINARY; PRT; 354 AA.
AC Q8LAY8
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Protein phosphatase 2C-like protein (Hypothetical protein).
GN AT5G10740/T30N20.10 OR AT5G10740.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurasids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation."
RL Genome Biol. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinozaki K.;
RT "Arabidopsis thaliana full-length cDNA."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;

"Arabidopsis Open Reading Frame (ORF) Clones";
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY087522; AAM65064.1; -
DR EMBL; AK117549; BAC42210.1; -
DR EMBL; BT005431; AAO63851.1; -
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004722; P:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C_SIC; 1.
DR PROSITE; PS00215; MITOCH_CARRIER; 1.
DR PROSITE; PS1032; PP2C; 1.
KW Hypothetical protein.
SQ SEQUENCE 354 AA; 38036 MW; 87DA535B561C9D68 CRC64;

Query Match 18.4%; Score 370.5; DB 10; Length 354;
Best Local Similarity 36.7%; Pred. No. 1.7e-21;
Matches 105; Conservative 47; Mismatches 87; Indels 47; Gaps 13;

QY 109 GYVAERKGEREMQD-AHVILNDITECRPPSSLIITVSYFAVFDGHHGIRASKFAAQN 167
DB 35 GY-ASSAGKRGSMEDFFETRIDNGEIT-----VGLFVFDGHHGARAAYVKRHL 84

QY 168 HONLIRKPKGDVLSVEKTVKRCILDTFKHTDEFLKQASSQKPAWK-GSTATCVLAVD 226
DB 85 FSNLI-THPK--FIS---DTKSAITDAYNHTDLSLLKSENHN---RDAGSTASTAILVG 135

QY 227 NILYANLGDRAILCRYNESQKHAALSLSKEHNPTQYERMRIOKAGNVN---DGRV 283
DB 136 DRLVAVNGDSRAVISRGK-----AIVSRDHKPDQSDERERENAGGVMMWAGTRV 199

QY 284 LGVLEVSISGQYKRGVTSVPDIRCOLTPNDRIILLACDGLFKVFTPEEAVNFILS 343
DB 190 GGVLAVSRAFGDRLKQY-VVADPEIQEIKDDTLEFLILASDGLWDVFSNEAAVMV-- 246

QY 344 CLEDEKIQTRGKSAADARYEAACNRLANKAVQSGADNVTVMVVR 389
DB 247 -----KEVEDP--EDSAKLVGEAIKRGSDNITCVVVR 278

RESULT 15
QBVZD9 PRELIMINARY; PRT; 420 AA.
AC QBVZD9;
DT 01-MAR-2002 (TREMELrel. 20, Created)
DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE AT5G53140/MFH8.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
[1]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cdna clones";
RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

[2]
SEQUENCE FROM N.A.
RP Cheuk R., Chen H., Kim C.J., Shinn P., Banh J., Bowser L.,
RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis ORF clones";
RT Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
DR EMBL; AY065026; AAL57666.1; -
DR EMBL; AY133656; AAM91486.1; -
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004722; P:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydrolase; Magnesium.
SQ SEQUENCE 420 AA; 45752 MW; 2DF6960D75BF9058 CRC64;

Query Match 18.3%; Score 368.5; DB 10; Length 420;
Best Local Similarity 32.8%; Pred. No. 3.1e-21;
Matches 112; Conservative 60; Mismatches 108; Indels 61; Gaps 13;

QY 64 TSISQVMTGEGKAKRKTSEENKNGSEELVEKKVKASSVIFGLK-----GVVAERK 115
DB 58 TSAKMWVDI-----SAGEKRISLVDMPPEKVDGGYIGGKNDGSLSCGYCSFR- 108

QY 116 GREEMQDAHVILNDITECRPPSSLIITVSYFAVFDGHHGIRASKFAAQNHLIRKF 175
DB 109 GKSTMEDFYDIKASTIEG-----QAVCMFGIFDGHGSSRAAEYLKHLFNLM-KH 159

QY 176 PKGDVISEKTVKRCILDTFKHTDEFLKQASSQKPAWK-DGSTATCVLAVDNLYIANL 234
DB 160 PQ-----FUTDTKLALNETYKQTDVAFLE---SEKDTRDDGSTASAAVLGNHLYVANV 211

QY 235 GDSRAILCRYNESQKHAALSLSKEHNPTQYERMRIOKAGNVN---DGRVLGVLVSR 291
DB 212 GDSRTIV-----SKAGKAIASLDDHKPNRSDEKRIESAGGVIMWAGTRVGGVLAWSR 265

QY 292 SIGDGOYKRGVTSVPDIRCOLTPNDRIILLACDGLFKVFTPEEAVNFILSCLDEKIQ 351
DB 266 ALGNRLKQF-VVABPEIQDLEIDHEALLVLASDGLWDVVDVNEADAV--ALAAQSEEP-- 320

QY 352 TREGKSAADARYEAACNRLANKAVQSGADNVTVMVVRIGH 392
DB 321 -----EAAARKLTDATFGRGSDNITCVVVRFRH 349

Search completed: April 12, 2004, 09:08:13
Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:00:56 ; Search time 58 seconds
(without alignments)
1909.631 Million cell updates/sec

Title: US-09-935-124A-2
Perfect score: 2018
Sequence: 1 MDLFGDLPEPESPRPAACK.....KAVQRGSADNTVMVVRIGH 392

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Watch 0%
Maximum Watch 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2018	100.0	392	AAB28791	Aab28791 Human hyd
2	2018	100.0	392	ABB05726	Abb05726 Human sig
3	2018	100.0	392	ABG73740	Abg73740 Human ILK
4	2018	100.0	392	ADB90823	Adb90823 Human hyd
5	2018	100.0	392	ADE55482	Ades5482 Human Pro
6	2018	100.0	392	ADE55454	Ades5454 Human Pro
7	2018	100.0	392	ADE55466	Ades5466 Human Pro
8	2018	100.0	392	ADE55458	Ades5458 Human Pro
9	2018	100.0	421	ABB12317	Abb12317 Human pro
10	2018	100.0	421	AAM40555	Aam40555 Human pol
11	2018	100.0	441	AAU23566	Aau23566 Novel hum
12	2018	100.0	446	AAU22933	Aau22933 Novel hum
13	2015	99.9	392	AAB92585	Aab92585 Human pro
14	2014	99.8	392	AAM38769	Aam38769 Human pol
15	1931	95.7	392	ADE55484	Ades5484 Rat Prote
16	1931	95.7	392	ADE55452	Ades5452 Rat Prote
17	1931	95.7	392	ADE55456	Ades5456 Rat Prote
18	1931	95.7	392	ADE55460	Ades5460 Rat Prote
19	1927	95.5	392	ABP72390	Abp72390 Rat prote
20	1457.5	72.2	378	ABG09937	Abg09937 Novel hum
21	928	46.0	221	ABG09936	Abg09936 Novel hum
22	533.5	26.4	211	ABG07619	Abg07619 Novel hum
23	447.5	22.2	138	AAU23252	Aau23252 Novel hum
24	431.5	21.4	295	AAG18068	Aag18068 Arabidops
25	431.5	21.4	305	AAG18067	Aag18067 Arabidops

ALIGNMENTS

RESULT 1

AAB28791
ID AAB28791 standard; protein; 392 AA.

XX	AC	AAB28791;			
XX	DT	13-FEB-2001 (first entry)			
XX	DE	Human hydrolase-like molecule 2 protein.			
XX	KW	Hydrolase-like molecule; human; cell proliferation disorder; autoimmune;			
XX	KW	cancer; AIDS; acquired immune deficiency syndrome.			
XX	OS	Homo sapiens.			
XX	PN	US6132964-A.			
XX	PD	17-OCT-2000.			
XX	PF	06-FEB-1998; 98US-00013881.			
XX	PR	06-FEB-1998; 98US-00013881.			
XX	PA	(INCY-) INCYTE PHARM INC.			
XX	PI	Bandman O, Hillman JL, Guegler KJ, Shah P, Lal P, Corley NC;			
XX	DR	WPI; 2001-006133/01.			
XX	DR	N-PSDB; AAC60224.			
XX	PT	New human hydrolase-like molecules (HHLMs) and polynucleotides encoding the HHLMs, useful for diagnosing, treating or preventing cell proliferation (e.g. bone cancer) or autoimmune disorders(e.g. AIDS or asthma).			
XX	PT	Claim 1; Col 43-46; 38pp; English.			
XX	PS	The present invention relates to isolated and purified cDNA encoding a human hydrolase-like molecule (HHLM), designated HHLM-1 to HHLM-8. The HHLM DNAs and polypeptides are useful for diagnosing, treating or preventing cell proliferation disorders and autoimmune disorders. Cell proliferation disorders include cancers, autoimmune disorders include AIDS (acquired immune deficiency syndrome). The present sequence is a HHLM protein of the invention			
XX	CC	Sequence 392 AA;			
XX	SQ	Query Match 100.0%; Score 2018; DB 4; Length 392;			

26	404	20.0	86	3	AAG03424	Aag03424 Human sec
27	395.5	19.6	274	5	ABB78060	Abb78060 Consensus
28	391.5	19.4	219	3	AAG18069	Aag18069 Arabidops
29	370.5	18.4	353	5	ABB77579	Abb77579 Physcomit
30	370.5	18.4	353	6	ABG74204	Abg74204 P. patens
31	370.5	18.4	354	3	AAG06997	Aag06997 Arabidops
32	366.5	18.2	360	3	AAG16902	Aag16902 Arabidops
33	366.5	18.2	383	3	AAG18039	Aag18039 Arabidops
34	366.5	18.2	420	3	AAG39774	Aag39774 Arabidops
35	366.5	18.2	454	5	ABB08398	Abb08398 Human-der
36	366.5	18.2	454	7	ADD89793	Add89793 Human FEM
37	364	18.0	358	3	AAG39776	Aag39776 Arabidops
38	364	18.0	358	3	AAG18041	Aag18041 Arabidops
39	364	18.0	359	3	AAG18040	Aag18040 Arabidops
40	363	18.0	359	3	AAG39775	Aag39775 Arabidops
41	358.5	17.8	361	5	ABB92620	Abb92620 Herpicida
42	358.5	17.8	361	6	ABP56903	Abp56903 Arabidops
43	358.5	17.8	361	6	ABP56904	Abp56904 Arabidops
44	358.5	17.8	361	6	ABP56902	Abp56902 Arabidops
45	358.5	17.8	361	6	ABP56902	Abp56902 Arabidops

Best Local Similarity 100.0%; Pred. No. 4.8e-186;
 Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDLFGDLPEPERSPPAAGKEAQKGLLFDLPPASSTDSGGPGLLFDLPPASSGDSG 60
 DB 1 MDLFGDLPEPERSPPAAGKEAQKGLLFDLPPASSTDSGGPGLLFDLPPASSGDSG 60
 QY 61 SLATSISQWVKTEGKAKRKTSEEEKNGSEBELVEKVKCKASSVIFGLKGYVAERKGEREE 120
 DB 61 SLATSISQWVKTEGKAKRKTSEEEKNGSEBELVEKVKCKASSVIFGLKGYVAERKGEREE 120
 QY 121 MODAHVILNDITECRPPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKFPKGDV 180
 DB 121 MODAHVILNDITECRPPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKFPKGDV 180
 QY 181 ISVEKTVKRCCLDTFKHTDEBFLKQASSQKPAWKDGGTATCVLAVDNTILYIANLGDSRAI 240
 DB 181 ISVEKTVKRCCLDTFKHTDEBFLKQASSQKPAWKDGGTATCVLAVDNTILYIANLGDSRAI 240
 QY 241 LCRYNESQKHAALSLSKEHNPTQYEERMRQKAGGNVRDGRVGLVLEVSRSIGDQYKR 300
 DB 241 LCRYNESQKHAALSLSKEHNPTQYEERMRQKAGGNVRDGRVGLVLEVSRSIGDQYKR 300
 QY 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
 DB 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
 QY 361 ARYEACNRLANKAVQSGADNVTVMVVRIGH 392
 DB 361 ARYEACNRLANKAVQSGADNVTVMVVRIGH 392

RESULT 2
 ABB05726
 ID ABB05726 standard; protein; 392 AA.
 AC ABB05726;
 XX
 DT 30-APR-2002 (first entry)
 DE Human signal transduction protein clone tes3_j1j20.
 KW Human; foetal brain; foetal kidney; melanoma; testis; amygdala;
 gene therapy.
 OS Homo sapiens.
 PN WO200198454-A2.
 XX
 PD 27-DEC-2001.
 XX
 PF 25-APR-2001; 2001WO-1B002050.
 XX
 PR 25-APR-2000; 2000US-0199380P.
 XX
 PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
 PI Wiemann S;
 XX
 XX WPI: 2002-055860/07.
 XX N-PSDB: ABQ77081.
 XX
 PT Human cDNA sequences and clones derived from human fetal brain, fetal
 kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic
 screening and therapy

QY 1 MDLFGDLPEPERSPPAAGKEAQKGLLFDLPPASSTDSGGPGLLFDLPPASSGDSG 60
 DB 1 MDLFGDLPEPERSPPAAGKEAQKGLLFDLPPASSTDSGGPGLLFDLPPASSGDSG 60
 QY 61 SLATSISQWVKTEGKAKRKTSEEEKNGSEBELVEKVKCKASSVIFGLKGYVAERKGEREE 120
 DB 61 SLATSISQWVKTEGKAKRKTSEEEKNGSEBELVEKVKCKASSVIFGLKGYVAERKGEREE 120
 QY 121 MODAHVILNDITECRPPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKFPKGDV 180
 DB 121 MODAHVILNDITECRPPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKFPKGDV 180
 QY 181 ISVEKTVKRCCLDTFKHTDEBFLKQASSQKPAWKDGGTATCVLAVDNTILYIANLGDSRAI 240
 DB 181 ISVEKTVKRCCLDTFKHTDEBFLKQASSQKPAWKDGGTATCVLAVDNTILYIANLGDSRAI 240
 QY 241 LCRYNESQKHAALSLSKEHNPTQYEERMRQKAGGNVRDGRVGLVLEVSRSIGDQYKR 300
 DB 241 LCRYNESQKHAALSLSKEHNPTQYEERMRQKAGGNVRDGRVGLVLEVSRSIGDQYKR 300
 QY 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
 DB 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
 QY 361 ARYEACNRLANKAVQSGADNVTVMVVRIGH 392
 DB 361 ARYEACNRLANKAVQSGADNVTVMVVRIGH 392

CC ABB05729. The human cDNA sequences and clones can be used in gene
 CC therapy. The clones may be used in a variety of applications, for example
 CC they may be used in profiling assays, for providing large arrays of human
 CC genetic material for implementing large-scale screening strategies and
 CC for treating diseases via gene therapy procedures
 XX
 SQ Sequence 392 AA;
 Query Match 100.0%; Score 2018; DB 5; Length 392;
 Best Local Similarity 100.0%; Pred. No. 4.8e-186;
 Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDLFGDLPEPERSPPAAGKEAQKGLLFDLPPASSTDSGGPGLLFDLPPASSGDSG 60
 DB 1 MDLFGDLPEPERSPPAAGKEAQKGLLFDLPPASSTDSGGPGLLFDLPPASSGDSG 60
 QY 61 SLATSISQWVKTEGKAKRKTSEEEKNGSEBELVEKVKCKASSVIFGLKGYVAERKGEREE 120
 DB 61 SLATSISQWVKTEGKAKRKTSEEEKNGSEBELVEKVKCKASSVIFGLKGYVAERKGEREE 120
 QY 121 MODAHVILNDITECRPPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKFPKGDV 180
 DB 121 MODAHVILNDITECRPPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKFPKGDV 180
 QY 181 ISVEKTVKRCCLDTFKHTDEBFLKQASSQKPAWKDGGTATCVLAVDNTILYIANLGDSRAI 240
 DB 181 ISVEKTVKRCCLDTFKHTDEBFLKQASSQKPAWKDGGTATCVLAVDNTILYIANLGDSRAI 240
 QY 241 LCRYNESQKHAALSLSKEHNPTQYEERMRQKAGGNVRDGRVGLVLEVSRSIGDQYKR 300
 DB 241 LCRYNESQKHAALSLSKEHNPTQYEERMRQKAGGNVRDGRVGLVLEVSRSIGDQYKR 300
 QY 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
 DB 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
 QY 361 ARYEACNRLANKAVQSGADNVTVMVVRIGH 392
 DB 361 ARYEACNRLANKAVQSGADNVTVMVVRIGH 392

RESULT 3
 ABB05740
 ID ABB05740 standard; protein; 392 AA.
 AC ABB05740;
 XX
 DT 27-MAR-2003 (first entry)
 DE Human ILKAP protein.
 KW ILKAP; integrin-linked kinase associated protein; C1 protein; human;
 angiogenesis; modulator; cell surface marker expression; gene therapy;
 avb3 integrin production; proliferation; differentiation.
 OS Homo sapiens.
 PN US2002156003-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 21-AUG-2001; 2001US-00935124.
 XX
 PR 18-APR-2001; 2001US-0284760P.
 XX
 PA (RIGE-) RIGEL PHARM INC.
 PI Lorens JB, Xu W, Atchison RE, Bogenberger J;
 XX
 XX WPI: 2003-182647/18.
 XX N-PSDB: ABQ77081.
 XX
 PT Identifying a compound that modulates angiogenesis, useful for monitoring

QY 1 MDLFGDLPEPERSPPAAGKEAQKGLLFDLPPASSTDSGGPGLLFDLPPASSGDSG 60
 DB 1 MDLFGDLPEPERSPPAAGKEAQKGLLFDLPPASSTDSGGPGLLFDLPPASSGDSG 60
 QY 61 SLATSISQWVKTEGKAKRKTSEEEKNGSEBELVEKVKCKASSVIFGLKGYVAERKGEREE 120
 DB 61 SLATSISQWVKTEGKAKRKTSEEEKNGSEBELVEKVKCKASSVIFGLKGYVAERKGEREE 120
 QY 121 MODAHVILNDITECRPPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKFPKGDV 180
 DB 121 MODAHVILNDITECRPPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKFPKGDV 180
 QY 181 ISVEKTVKRCCLDTFKHTDEBFLKQASSQKPAWKDGGTATCVLAVDNTILYIANLGDSRAI 240
 DB 181 ISVEKTVKRCCLDTFKHTDEBFLKQASSQKPAWKDGGTATCVLAVDNTILYIANLGDSRAI 240
 QY 241 LCRYNESQKHAALSLSKEHNPTQYEERMRQKAGGNVRDGRVGLVLEVSRSIGDQYKR 300
 DB 241 LCRYNESQKHAALSLSKEHNPTQYEERMRQKAGGNVRDGRVGLVLEVSRSIGDQYKR 300
 QY 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
 DB 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
 QY 361 ARYEACNRLANKAVQSGADNVTVMVVRIGH 392
 DB 361 ARYEACNRLANKAVQSGADNVTVMVVRIGH 392

PT changes in cell surface marker expression or avb3 integrin production,
PT comprises contacting the compound with an integrin-linked kinase
PT associated protein.

XX Example 1; Fig 1; 20pp; English.

XX This invention describes a novel compound that modulates angiogenesis
CC comprising contacting the compound with an integrin-linked kinase
CC associated protein (ILKAP) polypeptide, and determining the functional
CC effect of the compound on the ILKAP polypeptide. A method described in
CC the invention is useful for identifying modulators of angiogenesis, and
CC for monitoring changes in cell surface marker expression, avb3 integrin
CC production, proliferation and differentiation using either cell lines or
CC primary cells. The products of the invention can be used as ILKAP
CC modulators or for gene therapy. This sequence represents the human ILKAP
CC (also called C1 protein) describes in the disclosure of the invention

XX Sequence 392 AA;

XX Query Match 100.0%; Score 2018; DB 6; Length 392;
XX Best Local Similarity 100.0%; Pred. No. 4.8e-186;
XX Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPRAAGKEAQKGLLFDLPPASSTDSGGPILLFDLPPASSGDSG 60
DB 1 MDLFGDLPEPERSPPRAAGKEAQKGLLFDLPPASSTDSGGPILLFDLPPASSGDSG 60
QY 61 SLATSIQMWKTEGKAKRTISEEKNGSEELVEKKVKCASSVIFGLKGYVAERKGEREE 120
DB 61 SLATSIQMWKTEGKAKRTISEEKNGSEELVEKKVKCASSVIFGLKGYVAERKGEREE 120
QY 121 MQDAHVLNDITECPSPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKPKGDV 180
DB 121 MQDAHVLNDITECPSPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKPKGDV 180
QY 181 ISVEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGSRAI 240
DB 181 ISVEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGSRAI 240
QY 241 LCRYNEESQKHAALSLSKEHNPTQYEERMIQKAGNVDRGVLGVLEVSRSIGDQYKR 300
DB 241 LCRYNEESQKHAALSLSKEHNPTQYEERMIQKAGNVDRGVLGVLEVSRSIGDQYKR 300
QY 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
DB 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
QY 361 ARYEAAACNRLANKAVQSGSADNVTVMVVRIGH 392
DB 361 ARYEAAACNRLANKAVQSGSADNVTVMVVRIGH 392

RESULT 4

ID ADB90823

XX ADB90823 standard; protein; 392 AA.

XX AC ADB90823;

XX DT 04-DEC-2003 (first entry)

XX DE Human hydrolase-like molecule, HHLM 2, INCYTE 195647.

XX Human; hydrolase-like molecule; HHLM; cell proliferation disorder;
XX arteriosclerosis; atherosclerosis; bursitis; psoriasis; cancer;
XX autoimmune disorder; AIDS; Addison's disease;
XX adult respiratory distress syndrome; anaemia; asthma; diabetes mellitus.

XX OS Homo sapiens.

XX PN US6518029-B1.

XX PD 11-FEB-2003.

XX

PF 07-JUL-2000; 2000US-00612473.

XX 06-FEB-1998; 98US-00013881.

XX (INCY-) INCYTE GENOMICS INC.

XX Bandman O, Lal P, Hillman JL, Corley NC, Guegler KJ, Shah P;

XX WPI; 2003-742789/70.

XX N-PSDB; ADB90831.

XX New human hydrolase-like molecules, useful for treating or preventing
XX cell proliferation disorders (e.g. atherosclerosis or cancers) and
XX autoimmune disorders (e.g. AIDS, Addison's disease, anemia, asthma and
XX diabetes mellitus).

XX Claim 1; Fig 2; 55pp; English.

XX The invention relates to a new isolated polypeptide comprising a human
XX hydrolase-like molecule, termed HHLM-8 appearing as ADB90822 - ADB90829,
XX a naturally occurring polypeptide comprising a sequence which is at least
XX 81% identical the HHLM, a biologically active fragment of an HHLM or an
XX immunogenic fragment comprising at least 15 contiguous amino acids. Also
XX included are a composition comprising an HHLM and an excipient, a method
XX for screening a compound as an agonist or antagonist of HHLM (by exposing
XX a sample comprising HHLM to a compound, and detecting agonist or
XX antagonist activity in the sample), a method for screening a compound
XX that specifically binds to HHLM (by combining HHLM with at least one test
XX compound, and detecting binding of HHLM to the test compound) and a
XX method for screening a compound that modulates the activity of HHLM. The
XX human hydrolase-like molecules (HHLM), agonists and antagonists useful
XX for treating or preventing cell proliferation disorders (e.g.
XX arteriosclerosis, atherosclerosis, bursitis, psoriasis, and cancers) and
XX autoimmune disorders (e.g. AIDS, Addison's disease, adult respiratory
XX distress syndrome, anaemia, asthma and diabetes mellitus). The HHLM
XX polypeptides are useful in preparing antibodies that specifically bind to
XX the polypeptides. Nucleic acids encoding HHLM are useful in generating
XX probes for mapping naturally occurring genomic sequences, in detecting
XX differences in the chromosomal location due to translocation or
XX inversion, and in screening libraries of compounds in drug screening
XX techniques. The present sequence represents an HHLM of the invention.

XX Sequence 392 AA;

XX Query Match 100.0%; Score 2018; DB 7; Length 392;
XX Best Local Similarity 100.0%; Pred. No. 4.8e-186;
XX Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPRAAGKEAQKGLLFDLPPASSTDSGGPILLFDLPPASSGDSG 60
DB 1 MDLFGDLPEPERSPPRAAGKEAQKGLLFDLPPASSTDSGGPILLFDLPPASSGDSG 60
QY 61 SLATSIQMWKTEGKAKRTISEEKNGSEELVEKKVKCASSVIFGLKGYVAERKGEREE 120
DB 61 SLATSIQMWKTEGKAKRTISEEKNGSEELVEKKVKCASSVIFGLKGYVAERKGEREE 120
QY 121 MQDAHVLNDITECPSPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKPKGDV 180
DB 121 MQDAHVLNDITECPSPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKPKGDV 180
QY 181 ISVEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGSRAI 240
DB 181 ISVEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGSRAI 240
QY 241 LCRYNEESQKHAALSLSKEHNPTQYEERMIQKAGNVDRGVLGVLEVSRSIGDQYKR 300
DB 241 LCRYNEESQKHAALSLSKEHNPTQYEERMIQKAGNVDRGVLGVLEVSRSIGDQYKR 300
QY 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
DB 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
QY 361 ARYEAAACNRLANKAVQSGSADNVTVMVVRIGH 392

Query Match	100.0%	Score	2018;	DB	7;	Length	392;	
Best Local Similarity	100.0%;	Pred.	No. 4.8e-186;					
Matches	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	MDLFGDLPEPERSRPRPAAGKEAQKGLPLFDLDPASSTDSGGPLIFDDLPASSGDSG	60					
Db	1	MDLFGDLPEPERSRPRPAAGKEAQKGLPLFDLDPASSTDSGGPLIFDDLPASSGDSG	60					
QY	61	SLATSISOMWKTGKGARKTSEBKNGSEBELVKKYCKASSVIFGLKGYVAERGEREE	120					
Db	61	SLATSISOMWKTGKGARKTSEBKNGSEBELVKKYCKASSVIFGLKGYVAERGEREE	120					
QY	121	MDAHVIINDITEBCRPPSSLIITRVSPFAVFDGHHGIRASKFAAQNLHQLIRKFPKGDV	180					
Db	121	MDAHVIINDITEBCRPPSSLIITRVSPFAVFDGHHGIRASKFAAQNLHQLIRKFPKGDV	180					
QY	181	ISVETVKRCULDPTFKHTDEBFLQASSQKPAWKDGSATCVLADVNIILYIANTLGDSPAI	240					
Db	181	ISVETVKRCULDPTFKHTDEBFLQASSQKPAWKDGSATCVLADVNIILYIANTLGDSPAI	240					
QY	241	LCRYNEESQKHAALSLSKEHNPTQYEEMRITQKAGGNVRDGRVLGVLEVSRSIGDGQYKR	300					
Db	241	LCRYNEESQKHAALSLSKEHNPTQYEEMRITQKAGGNVRDGRVLGVLEVSRSIGDGQYKR	300					
QY	301	CGVTSVPDIRRCQLTPNDRPFIILLACDGLFKVFTPEEAVNFIISLCLEDEKIQITREGKSAAD	360					
Db	301	CGVTSVPDIRRCQLTPNDRPFIILLACDGLFKVFTPEEAVNFIISLCLEDEKIQITREGKSAAD	360					
QY	361	ARYEAACNRLANKAVQGSADNVTVMVVRIGH	392					
Db	361	ARYEAACNRLANKAVQGSADNVTVMVVRIGH	392					

RESULT 6	
ADE55454	
ID	ADE55454 standard; protein; 392 AA.
XX	
XX	ADE55454;
XX	AC
XX	AC
XX	29-JAN-2004 (first entry)
DT	
XX	
XX	Human Protein NP_110395, SEQ ID NO 1271.
DE	
XX	
XX	Human; pain; neuronal tissue; gene therapy;
KW	spinal segmental nerve injury; chronic constriction injury; CCI;
KW	spared nerve injury; SNI; Chung.
KW	

OS	Homo sapiens.
XX	
PN	WO2003016475-A2.
XX	
XX	
PD	27-FEB-2003.
XX	
XX	
PF	14-AUG-2002; 2002WO-US025765.
XX	
PR	14-AUG-2001; 2001US-0312147P.
PR	01-NOV-2001; 2001US-0346382P.
PR	26-NOV-2001; 2001US-0333347P.
XX	
PA	(GEHO) GEN HOSPITAL CORP.
PA	(FARB) BAYER AG.
XX	
PI	Woolf C, D'urso D, Befort K, Costigan M;
XX	
DR	WPI; 2003-268312/26.
DR	GENEANK; NP_110395.
XX	
PT	New composition comprising two or more isolated polypeptides, useful for
XX	preparing a medicament for treating pain in an animal.
PT	
XX	
PS	Claim 1; Page; 1017pp; English.
XX	

CC The invention discloses a composition comprising two or more isolated rat

Db	361	ARYEACNRLANKAVORGSAADNVTVMVVRIGH	392
RESULT 5			
ADE55462			
ID	ADE55462	standard; protein; 392 AA.	
XX	AC	ADE55462;	
XX	AC		
XX	DT	29-JAN-2004 (first entry)	
XX	XX		
DE	DE	Human Protein NP_110395, SEQ ID NO 1279.	
XX	XX		
KW	KW	Human; pain; neuronal tissue; gene therapy;	
KW	KW	spinal segmental nerve injury; chronic constriction injury; CCI;	
XX	XX	spared nerve injury; SNI; Chung.	
OS	OS	Homo sapiens.	
XX	XX		
PN	PN	WO2003016475-A2.	
XX	XX		
PD	PD	27-FEB-2003.	
XX	XX		
FF	FF	14-AUG-2002; 2002WO-US025765.	
XX	XX		
PR	PR	14-AUG-2001; 2001US-0312147P.	
PR	PR	01-NOV-2001; 2001US-0346382P.	
PR	PR	26-NOV-2001; 2001US-0333347P.	
XX	XX		
XX	XX	(GEHO) GEN HOSPITAL CORP.	
FA	FA	(FARB) BAYER AG.	
XX	XX		
PI	PI	Woolf C, D'urso D, Befort K, Costigan M;	
XX	XX		
DR	DR	WPI; 2003-268312/26.	
DR	DR	GENBANK; NP_110395.	
XX	XX		
PT	PT	New composition comprising two or more isolated polypeptides, useful for	
PT	PT	preparing a medicament for treating pain in an animal.	
XX	XX		
PS	PS	Claim 1; Page; 1017pp; English.	

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung)), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

XX
SQ Sequence 392 AA;

CC	or human polynucleotides or a polynucleotide which represents a fragment,	KW	spinal segmental nerve injury; chronic constriction injury; CCI;
CC	derivative or allelic variation of the nucleic acid sequence. Also	KW	spared nerve injury; SNI; Chung.
CC	claimed are a vector comprising the novel polynucleotide, a host cell	OS	Homo sapiens.
CC	comprising the vector, a method for identifying a nucleotide sequence	XX	WO2003016475-A2.
CC	which is differentially regulated in an animal subjected to pain and a	XX	27-FEB-2003.
CC	kit to perform the method, an array, a method for identifying an agent	PD	
CC	that increases or decreases the expression of the polynucleotide sequence	XX	
CC	that is differentially expressed in neuronal tissue of a first animal	XX	
CC	subjected to pain, a method for identifying a compound which regulates	PF	14-AUG-2002; 2002WO-US025765.
CC	the expression of a polynucleotide sequence which is differentially	XX	
CC	expressed in an animal subjected to pain, a method for identifying a	PR	14-AUG-2001; 2001US-0312147P.
CC	compound that regulates the activity of one or more of the	PR	01-NOV-2001; 2001US-0346382P.
CC	polynucleotides, a method for producing a pharmaceutical composition, a	PR	26-NOV-2001; 2001US-0333347P.
CC	method for identifying a compound or small molecule that regulates the	XX	(GEO) GEN HOSPITAL CORP.
CC	activity in an animal of one or more of the polypeptides given in the	PA	(FAR) BAYER AG.
CC	specification, a method for identifying a compound useful in treating	XX	
CC	pain and a pharmaceutical composition comprising the one or more	PI	Woolf C, D'urso D, Befort K, Costigan M;
CC	polypeptides or their antibodies. The polynucleotide or the compound that	XX	
CC	modulates its activity is useful for preparing a medicament for treating	XX	
CC	pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction	XX	
CC	injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene	XX	
CC	therapy). The sequence presented is a human protein (shown in table 2 of	DR	WPI: 2003-268312/26.
CC	the specification) which is differentially expressed during pain. Note:	DR	GENBANK: NP_110395.
CC	The sequence data for this patent did not form part of the printed	XX	
CC	specification, but was obtained in electronic form directly from WIPO at	PT	New composition comprising two or more isolated polypeptides, useful for
CC	ftp.wipo.int/pub/published_pct_sequences.	PT	preparing a medicament for treating pain in an animal.
XX		XX	
SQ	Sequence 392 AA;	PS	Claim 1; Page; 1017pp; English.
		XX	
		CC	The invention discloses a composition comprising two or more isolated rat
		CC	or human polynucleotides or a polynucleotide which represents a fragment,
		CC	derivative or allelic variation of the nucleic acid sequence. Also
		CC	claimed are a vector comprising the novel polynucleotide, a host cell
		CC	comprising the vector, a method for identifying a nucleotide sequence
		CC	which is differentially regulated in an animal subjected to pain and a
		CC	kit to perform the method, an array, a method for identifying an agent
		CC	that increases or decreases the expression of the polynucleotide sequence
		CC	that is differentially expressed in neuronal tissue of a first animal
		CC	subjected to pain, a method for identifying a compound which regulates
		CC	the expression of a polynucleotide sequence which is differentially
		CC	expressed in an animal subjected to pain, a method for identifying a
		CC	compound that regulates the activity of one or more of the
		CC	polynucleotides, a method for producing a pharmaceutical composition, a
		CC	method for identifying a compound or small molecule that regulates the
		CC	activity in an animal of one or more of the polypeptides given in the
		CC	specification, a method for identifying a compound useful in treating
		CC	pain and a pharmaceutical composition comprising the one or more
		CC	polypeptides or their antibodies. The polynucleotide or the compound that
		CC	modulates its activity is useful for preparing a medicament for treating
		CC	pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction
		CC	injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
		CC	therapy). The sequence presented is a human protein (shown in table 2 of
		CC	the specification) which is differentially expressed during pain. Note:
		CC	The sequence data for this patent did not form part of the printed
		CC	specification, but was obtained in electronic form directly from WIPO at
		CC	ftp.wipo.int/pub/published_pct_sequences.
		XX	
		SQ	Sequence 392 AA;
			Query Match 100.0%; Score 2018; DB 7; Length 392;
			Best Local Similarity 100.0%; Pred. No. 4.8e-186;
			Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MDLFGDLPEPERSPPRPAAGKEAQKGLLFDLLPPASSTDSGSGPLFLDPLPPASGDSG 60		
Db	1 MDLFGDLPEPERSPPRPAAGKEAQKGLLFDLLPPASSTDSGSGPLFLDPLPPASGDSG 60		
Qy	61 SLATSIQWVKTEGKAKRTSEEEKNGSEELVEKVKCKASSVIFGLKGYVAERKGEREE 120		
Db	61 SLATSIQWVKTEGKAKRTSEEEKNGSEELVEKVKCKASSVIFGLKGYVAERKGEREE 120		
Qy	121 MQDAHVLNDITECRPPSSLLITRVSFAVFDHGGIRASKFAAQNHLIRKPKGDV 180		
Db	121 MQDAHVLNDITECRPPSSLLITRVSFAVFDHGGIRASKFAAQNHLIRKPKGDV 180		
Qy	181 ISVEKTVKRCLLDTFKTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGSRAI 240		
Db	181 ISVEKTVKRCLLDTFKTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGSRAI 240		
Qy	241 LCRYNESQKHAALSLSKEHNPTQYERMRIOKAGNVDRGVLTGVLEVSRSIGDGQYKR 300		
Db	241 LCRYNESQKHAALSLSKEHNPTQYERMRIOKAGNVDRGVLTGVLEVSRSIGDGQYKR 300		
Qy	301 CGVTSVPDIRRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360		
Db	301 CGVTSVPDIRRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360		
Qy	361 ARYBAACNRLANKAVQSGSADNVTVVVRIGH 392		
Db	361 ARYBAACNRLANKAVQSGSADNVTVVVRIGH 392		
RESULT 7			
AD55466			
ID	AD55466 standard; protein; 392 AA.		
XX			
AC	AD55466;		
XX			
DT	29-JAN-2004 (first entry)		
XX			
DE	Human Protein NP_110395, SEQ ID NO 1283.		
XX			
KW	Human; pain; neuronal tissue; gene therapy;		

Qy	1 MDLFGDLPEPERSPPRPAAGKEAQKGLLFDLLPPASSTDSGSGPLFLDPLPPASGDSG 60		
Db	1 MDLFGDLPEPERSPPRPAAGKEAQKGLLFDLLPPASSTDSGSGPLFLDPLPPASGDSG 60		
Qy	61 SLATSIQWVKTEGKAKRTSEEEKNGSEELVEKVKCKASSVIFGLKGYVAERKGEREE 120		
Db	61 SLATSIQWVKTEGKAKRTSEEEKNGSEELVEKVKCKASSVIFGLKGYVAERKGEREE 120		
Qy	121 MQDAHVLNDITECRPPSSLLITRVSFAVFDHGGIRASKFAAQNHLIRKPKGDV 180		
Db	121 MQDAHVLNDITECRPPSSLLITRVSFAVFDHGGIRASKFAAQNHLIRKPKGDV 180		

Query Match 100.0%; Score 2018; DB 7; Length 392;
Best Local Similarity 100.0%; Pred. No. 4.8e-186;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the

RESULT 9
 ABB12317
 ID ABB12317 standard; peptide; 421 AA.
 XX
 AC ABB12317;
 XX
 XX
 DT 11-JAN-2002 (first entry)
 XX
 XX
 DE Human protein phosphatase 2C homologue, SEQ ID NO:2687.

KW	Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW	haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW	inhibit; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW	proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW	myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW	chronic inflammatory condition; proliferative retinopathy;
KW	atherosclerosis; coronary heart disease; arterial ischaemia;
KW	bone disorder; osteoporosis; vascular growth disorder; immune
KW	tissue regeneration; wound healing; infection; immune disorder;
KW	cell culture; drug screening; gene therapy; antiinflammatory;
KW	antiasthmatic; antiarthritis; haemostatic; antiarteriosclerotic;
KW	cytostatic; osteopathic; vasoprotic; cardiant; virucide; antibacterial;
KW	antifungal; vulnery; antiulcer.
XX	
XX	
OS	Homo sapiens.

PN WO200157188-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US003800.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 XX
 PR 27-APR-2000; 2000US-00560875.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-457740/49.
 XX
 DR N-PSDB; ABA09561.
 XX
 DR Human proteins and DNA encoding sequences useful for preventing, treating
 PT and ameliorating a medical condition in a mammalian subject e.g. arthritis
 PT and cancer.
 XX
 PS Claim 20; Page 330; 1563pp; English.
 XX
 CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoietic regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention
 XX
 SQ Sequence 421 AA;
 Query Match 100.0%; Score 2018; DB 4; Length 421;
 Best Local Similarity 100.0%; Pred. No. 5.3e-186;
 Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDLFGDLPEPERSPPAAGKEAQKGLLFDLLPASTDSTGSGGGLLFDLLPASTGDSG 60
 DB 1 MDLFGDLPEPERSPPAAGKEAQKGLLFDLLPASTDSTGSGGGLLFDLLPASTGDSG 89
 QY 61 SLATISQMKVTEGKAGKRTSEBKNGSELVEKKVKCKASSVIFGLKGYVAERKEREE 120
 DB 90 SLATISQMKVTEGKAGKRTSEBKNGSELVEKKVKCKASSVIFGLKGYVAERKEREE 149

QY 121 MQDAHVILNDITECRPPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKPKGDV 180
 DB 150 MQDAHVILNDITECRPPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKPKGDV 209
 QY 181 ISVEKTVKRCLLDTFKETDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDRAI 240
 DB 210 ISVEKTVKRCLLDTFKETDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDRAI 269
 QY 241 LCRYNESQKHAALSLSKEHNPTQYERMRIOKAGNVDRGVGLVLEVSRSIGDGYKR 300
 DB 270 LCRYNESQKHAALSLSKEHNPTQYERMRIOKAGNVDRGVGLVLEVSRSIGDGYKR 329
 QY 301 CGVTSVPDIRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRREGKSAAD 360
 DB 330 CGVTSVPDIRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRREGKSAAD 389
 QY 361 ARYEACNRLANKAVQSGADNVTVMVRIGH 392
 DB 390 ARYEACNRLANKAVQSGADNVTVMVRIGH 421
 RESULT 10
 AAM40555
 ID AAM40555 standard; protein; 421 AA.
 XX
 AC AAM40555;
 XX
 DT 22-OCT-2001 (first entry)
 DE Human polypeptide SEQ ID NO 5486.
 XX
 KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US034263.
 XX
 PR 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-00552317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00620312.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI; 2001-442253/47.
 DR N-PSDB; AAI59711.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.
 XX
 PS Example 2; SEQ ID NO 5486; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
 CC encoded polypeptides (AAM38642-AAM42213) with nootropic,

Novel polypeptides and polynucleotides useful for diagnosing, preventing, PT
XX

XX Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
 XX ligase; hyperproliferative disorder; immunodeficiency disorder;
 XX autoimmune disorder; neurological disorder; metabolic disorder;
 XX inflammatory disorder; cardiovascular disorder; reproductive disorder;

Sequence 441 AA;

Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Novel human enzyme polypeptide #19.

XX Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
 XX ligase; hyperproliferative disorder; immunodeficiency disorder;
 XX autoimmune disorder; neurological disorder; metabolic disorder;
 XX inflammatory disorder; cardiovascular disorder; reproductive disorder;

PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI: 2001-465566/50.
XX N-PSDB; AAS40803.
XX Novel polypeptides and polynucleotides useful for diagnosing, preventing,
PT treating neural, immune system, muscular, reproductive, pulmonary,
PT cardiovascular, renal, proliferative disorders and cancerous diseases.
XX Claim 11; SEQ ID NO 929; 1180pp; English.
XX The present invention relates to the isolation of novel human enzyme
CC polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences
CC encoding them. The enzyme polypeptides of the invention may comprise the
CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC isomerases or ligases. The sequences of the invention are useful in the
CC diagnosis, treatment, prevention and/or prognosis of a wide range of
CC disorders including hyperproliferative disorders (e.g. cancer),
CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
CC arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic
CC disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),
CC cardiovascular disorders (e.g. atherosclerosis), blood-related disorders
CC (e.g. haemophilia), reproductive disorders (e.g. infertility) and
CC infectious disorders (e.g. Influenza). The polynucleotides of the
CC invention can also be used in gene therapy. AAU22915-AAU23814 represent
CC the novel human enzyme polypeptides of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
XX Sequence 446 AA;
Query Match 100.0%; Score 2018; DB 4; Length 446;
Best Local Similarity 100.0%; Pred. No. 5.8e-186;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDLFGDLPPEPRSPRPAAGKEAQKGPLLFDLPPASSTDSGGPGLLFDLPPASGDSG 60
Db 55 MDLFGDLPPEPRSPRPAAGKEAQKGPLLFDLPPASSTDSGGPGLLFDLPPASGDSG 114
Qy 61 SLATSISQVMTKTEGKAKRTSEEEKNGSELVEKVKYKASSVIFGLKGYVAERGEREE 120
Db 115 SLATSISQVMTKTEGKAKRTSEEEKNGSELVEKVKYKASSVIFGLKGYVAERGEREE 174
Qy 121 MDAHVILNDITECRPPSSLITRVSYFAVFDGHHGIRASGKFAAQNHLIRKFKGDV 180
Db 175 MDAHVILNDITECRPPSSLITRVSYFAVFDGHHGIRASGKFAAQNHLIRKFKGDV 234
Qy 181 ISVEKTVKRCLLDTFKHTDEEFLQAASSQKPAWKDGTATCVLAVDNILYIANLGSRAI 240
Db 235 ISVEKTVKRCLLDTFKHTDEEFLQAASSQKPAWKDGTATCVLAVDNILYIANLGSRAI 294
Qy 241 LCRYNESQKHAALSLSKEHNPTQYERMRIQKAGNVNDRGVLGVLVRSRIGDQGYKR 300
Db 295 LCRYNESQKHAALSLSKEHNPTQYERMRIQKAGNVNDRGVLGVLVRSRIGDQGYKR 354
Qy 301 CGVTSVPDIRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKICTREGKSAAD 360
Db 355 CGVTSVPDIRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKICTREGKSAAD 414
Qy 361 ARYEAAACNRLANKAVORGADNVTVVVRIGH 392
Db 415 ARYEAAACNRLANKAVORGADNVTVVVRIGH 446
RESULT 13
AAB92585
ID AAB92585 standard; protein; 392 AA.
XX

AC AAB92585;
XX 26-JUN-2001 (first entry)
DT Human protein sequence SEQ ID NO:10816.
DE Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX Homo sapiens.
XX EP1074617-A2.
XX 07-FEB-2001.
XX 28-JUL-2000; 2000EP-00116126.
XX 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX (HELI-) HELIX RES INST.
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI: 2001-318749/34.
XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
XX
XX Claim 8; SEQ ID NO 10816; 2537pp + Sequence Listing; English.
XX The present invention describes primer sets for synthesizing 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dr primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
XX Sequence 392 AA;
Query Match 99.9%; Score 2015; DB 4; Length 392;
Best Local Similarity 99.7%; Pred. No. 9.3e-186;
Matches 391; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDLFGDLPPEPRSPRPAAGKEAQKGPLLFDLPPASSTDSGGPGLLFDLPPASGDSG 60
Db 1 MDLFGDLPPEPRSPRPAAGKEAQKGPLLFDLPPASSTDSGGPGLLFDLPPASGDSG 60
Qy 61 SLATSISQVMTKTEGKAKRTSEEEKNGSELVEKVKYKASSVIFGLKGYVAERGEREE 120
Db 61 SLATSISQVMTKTEGKAKRTSEEEKNGSELVEKVKYKASSVIFGLKGYVAERGEREE 120

QY 121 MODAHVILNDITECRPPSSLIITRVSFAVFDGGHGIKASFAAQNHLHONLIRKPPKGDV 180
Db 121 MODAHVILNDITECRPPSSLIITRVSFAVFDGGHGIKASFAAQNHLHONLIRKPPKGDV 180
QY 181 ISVEKTVKRCCLDTFKHTDEEFLKQASSQKPAWKDGSATCFLAVDNILYIANLGDSRAI 240
Db 181 ISVEKTVKRCCLDTFKHTDEEFLKQASSQKPAWKDGSATCFLAVDNILYIANLGDSRAI 240
QY 241 LCRYNESQKHAALSLSKEHNPTQYEERMRIOKAGNVRDGRVLGVLEVSRSIGDGOYKR 300
Db 241 LCRYNESQKHAALSLSKEHNPTQYEERMRIOKAGNVRDGRVLGVLEVSRSIGDGOYKR 300
QY 301 CGVTSVPDIRRCQLTNPDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
Db 301 CGVTSVPDIRRCQLTNPDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
QY 361 ARYEAAACNRLANKAVQSGADNVTVMVVRIGH 392
Db 361 ARYEAAACNRLANKAVQSGADNVTVMVVRIGH 392
RESULT 14
AAM38769
ID AAM38769 standard; protein; 392 AA.
XX
AC AAM38769;
XX
DT 22-OCT-2001 (first entry)
DE Human polypeptide SEQ ID NO 1914.
XX
KW Human; neotropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokineic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI: 2001-442253/47.
DR N-PSDB; AAI57925.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Example 3; SEQ ID NO 1914; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with neotropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful

CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 392 AA;
Query Match 99.8%; Score 2014; DB 4; Length 392;
Best Local Similarity 99.7%; Pred. No. 1.2e-185;
Matches 391; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLFGDLPEPERSPPRPAAGKEAQKGPLLFDLPPASSSTDGSGGPLLFDLPPASSGDSG 60
Db 1 MDLFGDLPEPERSPPRPAAGKEAQKGPLLFDLPPASSSTDGSGGPLLFDLPPASSGDSG 60
QY 61 SLATSISQMVKTGEGKAKRTSEEEKNGSEELVEKVKCKASSVIFGLKGYVAERKGEREE 120
Db 61 SLATSISQMVKTGEGKAKRTSEEEKNGSEELVEKVKCKASSVIFGLKGYVAERKGEREE 120
QY 121 MQDAHVILNDITECRPPSSLIITRVSFAVFDGGHGIKASFAAQNHLHONLIRKPPKGDV 180
Db 121 MQDAHVILNDITECRPPSSLIITRVSFAVFDGGHGIKASFAAQNHLHONLIRKPPKGDV 180
QY 181 ISVEKTVKRCCLDTFKHTDEEFLKQASSQKPAWKDGSATCFLAVDNILYIANLGDSRAI 240
Db 181 ISVEKTVKRCCLDTFKHTDEEFLKQASSQKPAWKDGSATCFLAVDNILYIANLGDSRAI 240
QY 241 LCRYNESQKHAALSLSKEHNPTQYEERMRIOKAGNVRDGRVLGVLEVSRSIGDGOYKR 300
Db 241 LCRYNESQKHAALSLSKEHNPTQYEERMRIOKAGNVRDGRVLGVLEVSRSIGDGOYKR 300
QY 301 CGVTSVPDIRRCQLTNPDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
Db 301 CGVTSVPDIRRCQLTNPDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
QY 361 ARYEAAACNRLANKAVQSGADNVTVMVVRIGH 392
Db 361 ARYEAAACNRLANKAVQSGADNVTVMVVRIGH 392
RESULT 15
ADE55464
ID ADE55464 standard; protein; 392 AA.
XX
AC ADE55464;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein AAC97497, SEQ ID NO 1281.
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX

PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
DR GENBANK; AAC97497.
XX
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX

Db 361 ARYEACNRLANKAVQSGADNVTVMVRIGH 392

Search completed: April 12, 2004, 09:06:13
Job time : 61 secs

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 392 AA;

Query Match		95.7%;	Score 1931;	DB 7;	Length 392;
Best Local Similarity		95.2%;	Pred. No. 1.2e-177;		
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Db	1	MDLFGDLPEPERPRPAAGKEAGGVLFDLPPASGSDSGGGLLFDLPPASGSDSG 60			
Qy	61	SLATSIQVMKTEGKAKRTSBEENKNGSEELVEKKVKKASSVIFGLKGVVAERKGEREE 120			
Db	61	SLATSGSQVKNEGKAKRKAPBEERNGGSEELVEKKVKKASSVIFGLKGVVAERKGEREE 120			
Qy	121	MQDAHVILNDITECRPPSLITRVSYFAVFDGHHGIRASKFAAQNLHQLIRKFKPGDV 180			
Db	121	MQDAHVILNDITECRPPSLITRVSYFAVFDGHHGIRASKFAAQNLHQLIRKFKPGDV 180			
Qy	181	ISVEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDRAI 240			
Db	181	ISVEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDRAI 240			
Qy	241	LCRYNESQKHAALSLSKEHNPTQYERMERIQAGNVRDGRVGLVLEVSRSIGDQYKR 300			
Db	241	LCRYNESQKHAALSLSKEHNPTQYERMERIQAGNVRDGRVGLVLEVSRSIGDQYKR 300			
Qy	301	CGVTSVPDIERCOLTPNDRIILLACDGLFKVFTPEEAVNFILSCLEDEKIQIREKSAAD 360			
Db	301	CGVTSVPDIERCOLTPNDRIILLACDGLFKVFTPEEAVNFILSCLEDEKIQIREKSAAD 360			
Qy	361	ARYEACNRLANKAVQSGADNVTVMVRIGH 392			

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:07:23 ; Search time 46 Seconds
(without alignments)

2240.689 Million cell updates/sec

Title: US-09-935-124A-2

Perfect score: 2018
Sequence: 1 MDLFGDLPEPERSPPRAAGK.....KAVRGSDNVTVVVRIGH 392

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1073127 seqs, 262937947 residues

Total number of hits satisfying chosen parameters: 1073127

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2018	100.0	392	9	US-09-935-124A-2
2	2018	100.0	392	14	US-10-359-499-2
3	2018	100.0	421	12	US-10-276-774-2697
4	1927	95.5	392	14	US-10-218-137-22
5	1277	63.3	248	14	US-10-147-874-3
6	422.5	20.9	260	12	US-10-072-012-853
7	421.5	20.9	300	14	US-10-170-789-35
8	403.5	20.0	252	12	US-10-072-012-854
9	403.5	20.0	338	12	US-10-424-599-226401
10	403.5	20.0	338	12	US-10-424-599-226412
11	399.5	19.8	314	12	US-10-424-599-219869
12	397.5	19.7	312	12	US-10-424-599-219880
13	395.5	19.6	274	9	US-09-860-351-4
14	388	19.2	371	12	US-10-425-114-66152
15	386	19.1	333	12	US-10-425-114-62620

16	374	18.5	310	12	US-10-425-114-50324	Sequence 50324, A
17	374	18.5	310	12	US-10-425-114-60282	Sequence 60282, A
18	373	18.5	310	12	US-10-425-114-46846	Sequence 46846, A
19	371.5	18.4	416	12	US-10-425-114-59347	Sequence 59347, A
20	370.5	18.4	353	9	US-09-828-302-14	Sequence 14, Appl
21	369.5	18.3	416	12	US-10-425-114-72766	Sequence 72766, A
22	362.5	18.0	334	12	US-10-425-114-63384	Sequence 63384, A
23	362.5	18.0	343	12	US-10-425-114-67289	Sequence 67289, A
24	359.5	17.8	379	12	US-10-425-114-55704	Sequence 55704, A
25	358.5	17.8	345	12	US-10-425-114-65340	Sequence 65340, A
26	358.5	17.8	361	14	US-10-178-977A-2	Sequence 2, Appli
27	358.5	17.8	361	14	US-10-178-977A-4	Sequence 4, Appli
28	358.5	17.8	361	14	US-10-178-977A-6	Sequence 6, Appli
29	356.5	17.7	356	12	US-10-425-114-39847	Sequence 39847, A
30	354	17.5	356	12	US-10-424-599-208454	Sequence 208454, A
31	353.5	17.5	434	14	US-10-171-404A-46	Sequence 46, Appl
32	353.5	17.5	438	12	US-09-816-277-10	Sequence 10, Appl
33	353	17.5	383	12	US-10-424-599-191145	Sequence 191145, A
34	353	17.5	400	12	US-10-425-114-46211	Sequence 46211, A
35	352.5	17.5	370	12	US-10-425-114-69654	Sequence 69654, A
36	352.5	17.5	375	12	US-10-425-114-63857	Sequence 63857, A
37	352	17.4	482	12	US-10-425-114-58868	Sequence 58868, A
38	350	17.3	339	12	US-10-425-114-43779	Sequence 43779, A
39	349.5	17.3	360	12	US-10-425-114-70158	Sequence 70158, A
40	348.5	17.3	455	15	US-10-108-260A-4628	Sequence 4628, Ap
41	348	17.2	370	15	US-10-369-493-22760	Sequence 22760, A
42	347.5	17.2	528	12	US-10-425-114-40731	Sequence 40731, A
43	347.5	17.2	595	12	US-10-424-599-248091	Sequence 248091, A
44	347	17.2	348	15	US-10-369-493-5704	Sequence 5704, Ap
45	346.5	17.2	396	12	US-10-425-114-58998	Sequence 58998, A

ALIGNMENTS

RESULT 1
US-09-935-124A-2
; Sequence 2, Application US/09935124A
; Patent No. US20020156003A1
; GENERAL INFORMATION:
; APPLICANT: Lorens, James
; APPLICANT: Xu, Weiduan
; APPLICANT: Atchison, Robert
; APPLICANT: Bogenberger, Jakob
; TITLE OF INVENTION: Modulators of Angiogenesis
; FILE REFERENCE: 021044-000210us
; CURRENT APPLICATION NUMBER: US/09/935.124A
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: 60/284,760
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-124A-2

Query Match	100.0%	Score 2018;	DB 9;	Length 392;
Best Local Similarity	100.0%;	Pred. No. 3.1e-181;		
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DB	1	MDLFGDLPEPERSPPRAAGKQAQKGLFLDLPASSTDSGGPGLLFDLPASSGDSG	60	
QY	61	SLATISQWVTEGKAKRTSEEEKNGSEELVEKVKCASSVIFGLGYVAERKGEREE	120	
DB	61	SLATISQWVTEGKAKRTSEEEKNGSEELVEKVKCASSVIFGLGYVAERKGEREE	120	
QY	121	MODAHVILNDITECRPPSSLIITRVSYFAVFDGHHGIRASKFAAQLHONLIRKPKGDV	180	
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QY 301 CGVTSVPDIRRQCLTNDPFRILLACDGLFKVFTPEAVNFILSCLEDEKIQTRGKSAAD 360
DB 301 CGVTSVPDIRRQCLTNDPFRILLACDGLFKVFTPEAVNFILSCLEDEKIQTRGKSAAD 360
QY 361 ARYEACNRLANKAVQSGADNVTVVVRIGH 392
DB 361 ARYEACNRLANKAVQSGADNVTVVVRIGH 392

RESULT 2

US-10-359-499-2
; Sequence 2, Application US/10359499
; Publication No. US20030148363A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
; FILE REFERENCE: PF-0470-1 CIP
; CURRENT APPLICATION NUMBER: US/10/359,499
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/612,473
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/013,881
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030148363A1 195647
US-10-359-499-2

Query Match 100.0%; Score 2018; DB 14; Length 392;
Best Local Similarity 100.0%; Pred. No. 3.1e-181;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPAAGKEAQKGLLFDLLPPASSTDSGGGPLELFDLLPPASSGDSG 60
DB 1 MDLFGDLPEPERSPPAAGKEAQKGLLFDLLPPASSTDSGGGPLELFDLLPPASSGDSG 60
QY 61 SLATSISQMVKTGKAKKTSSEENKNGSEELVEKVKCKASSVIFGLKGYVAERKGEREE 120
DB 61 SLATSISQMVKTGKAKKTSSEENKNGSEELVEKVKCKASSVIFGLKGYVAERKGEREE 120
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DB 121 MQDAHVLNDITEECRPPSSLTITRVSFAVFDGHHGIRASKFAAQNHLIRKFKPGDV 180
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DB 181 ISVEKTVKRCCLDTPFKHTDEEFLKQASSQKPAWKDGGSTATCVLAVDNILYIANLGDRAI 240
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DB 301 CGVTSVPDIRRQCLTNDPFRILLACDGLFKVFTPEAVNFILSCLEDEKIQTRGKSAAD 360
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DB 361 ARYEACNRLANKAVQSGADNVTVVVRIGH 392
RESULT 3
US-10-276-774-2687
; Sequence 2687, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2687
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-2687

Query Match 100.0%; Score 2018; DB 12; Length 421;
Best Local Similarity 100.0%; Pred. No. 3.4e-181;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPAAGKEAQKGLLFDLLPPASSTDSGGGPLELFDLLPPASSGDSG 60
DB 30 MDLFGDLPEPERSPPAAGKEAQKGLLFDLLPPASSTDSGGGPLELFDLLPPASSGDSG 89
QY 61 SLATSISQMVKTGKAKKTSSEENKNGSEELVEKVKCKASSVIFGLKGYVAERKGEREE 120
DB 90 SLATSISQMVKTGKAKKTSSEENKNGSEELVEKVKCKASSVIFGLKGYVAERKGEREE 149
QY 121 MQDAHVLNDITEECRPPSSLTITRVSFAVFDGHHGIRASKFAAQNHLIRKFKPGDV 180
DB 150 MQDAHVLNDITEECRPPSSLTITRVSFAVFDGHHGIRASKFAAQNHLIRKFKPGDV 209
QY 181 ISVEKTVKRCCLDTPFKHTDEEFLKQASSQKPAWKDGGSTATCVLAVDNILYIANLGDRAI 240
DB 210 ISVEKTVKRCCLDTPFKHTDEEFLKQASSQKPAWKDGGSTATCVLAVDNILYIANLGDRAI 269
QY 241 LCRYNEESQKHAALSLSKEHNPTQYEEWRMRIOKAGNVRDGRVLGVLEVSRSIGDGQYKR 300
DB 270 LCRYNEESQKHAALSLSKEHNPTQYEEWRMRIOKAGNVRDGRVLGVLEVSRSIGDGQYKR 329
QY 301 CGVTSVPDIRRQCLTNDPFRILLACDGLFKVFTPEAVNFILSCLEDEKIQTRGKSAAD 360
DB 330 CGVTSVPDIRRQCLTNDPFRILLACDGLFKVFTPEAVNFILSCLEDEKIQTRGKSAAD 389
QY 361 ARYEACNRLANKAVQSGADNVTVVVRIGH 392
DB 390 ARYEACNRLANKAVQSGADNVTVVVRIGH 421

RESULT 4

US-10-218-137-22
; Sequence 22, Application US/10218137
; Publication No. US20030171255A1
; GENERAL INFORMATION:
; APPLICANT: Greengard, Paul
; APPLICANT: Svenningsson, Per
; APPLICANT: Rakhilin, Sergey
; APPLICANT: Starkova, Natalia

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATION OF DARPP-32 PHOSPHORYLATION
; FILE REFERENCE: 11181-005
; CURRENT APPLICATION NUMBER: US/10/218,137
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 60/311,641
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 22
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-10-218-137-22

Query Match 95.5%; Score 1927; DB 14; Length 392;
Best Local Similarity 94.9%; Pred. No. 1.2e-172;
Matches 372; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPEPRPAAAGKAEQKGLLFDLPPASSTDSGGPGLLFDLPPASSGDSG 60
DB 1 MDLFGDLPEPEPRPAAAGKAEQKGLLFDLPPASSTDSGGPGLLFDLPPASSGDSG 60

QY 61 SLATISQMVTEGKAGKRTSEKNGSSELVEKVKCKASSVIFGLKGVVAERKGEREE 120
DB 61 SLATSGSVVKNKGAKRKAPBEDNGGBELVEKVKCKASSVIFGLKGVVAERKGEREE 120

QY 121 MODAHVILNDITECRPPSSLIITVSVYFAVFDGGHGGIRASKFAAQNHLQNLIRKFKGVDV 180
DB 121 MODAHVILNDITQCNPPSSLIITVSVYFAVFDGGHGGIRASKFAAQNHLQNLIRKFKGVDV 180

QY 181 ISVEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDSPRAI 240
DB 181 ISVEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDSPRAI 240

QY 241 LCRYNEESQKHAALSLSKEHNFTQYEEERMRIQKAGNVDRGVLGVLEVSRSIGDQYKR 300
DB 241 LCRYNEESQKHAALSLSKEHNFTQYEEERMRIQKAGNVDRGVLGVLEVSRSIGDQYKR 300

QY 301 CGVTSVPDIRCQLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
DB 301 CGVTSVPDIRCQLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKPAVD 360

QY 361 ARYEACNRLANKAVQSGADNVTVMVRIGH 392
DB 361 ARYEACNRLANKAVQSGADNVTVMVRIGH 392

RESULT 5
; US-10-147-874-3
; Sequence 3, Application US/10147874
; Publication No. US20030027237A1
; GENERAL INFORMATION:
; APPLICANT: TARDIEUX, ISABELLE
; APPLICANT: DELORME, VIOLAINE
; TITLE OF INVENTION: SERINE-THREONINE PHOSPHATASE PROTEIN OF A PARASITIC ORGANISM OF T
; FILE REFERENCE: 223316US0
; CURRENT APPLICATION NUMBER: US/10/147,874
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 60/291,609
; PRIOR FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-147-874-3

Query Match 63.3%; Score 1277; DB 14; Length 248;
Best Local Similarity 100.0%; Pred. No. 1e-111;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 LITRVSYFAVFDGGHGGIRASKFAAQNHLQNLIRKFKGVDVISEKTVKRCLLDTFKHTDE 200
DB 1 LITRVSYFAVFDGGHGGIRASKFAAQNHLQNLIRKFKGVDVISEKTVKRCLLDTFKHTDE 60

QY 201 EFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDSPAILCRYNEESQKHAALSLSKEH 260
DB 61 EFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDSPAILCRYNEESQKHAALSLSKEH 120

QY 261 NPTQYEERMRIQKAGNVDRGVLGVLEVSRSIGDQYKRCGVTSPPIRRCOLTPNDRF 320
DB 121 NPTQYEERMRIQKAGNVDRGVLGVLEVSRSIGDQYKRCGVTSPPIRRCOLTPNDRF 180

QY 321 ILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAADARYEACNRLANKAVQSGA 380
DB 181 ILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAADARYEACNRLANKAVQSGA 240

QY 381 DNVTVMVV 388
DB 241 DNVTVMVV 248

RESULT 6
; US-10-072-012-853
; Sequence 853, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerrhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08

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/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1391
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 853
/ LENGTH: 260
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
/ OTHER INFORMATION: Serine/threonine phosphatases, family 2C,
/ OTHER INFORMATION: catalytic domain
US-10-072-012-853

Query Match          20.9%; Score 422.5; DB 12; Length 260;
Best Local Similarity 36.4%; Pred. No. 3.5e-31;
Matches 103; Conservative 56; Mismatches 93; Indels 31; Gaps 6;

QY 106 GLKGVVAERKGEREMQDAHVILNDITECPSPSSLITRVSYFAVFDGHHGIRASKFAAQ 165
Db 9 GLRYKSSMQGVKRPMDAHVITDLSGE-----DSGCFGVFDGHHGSEAAKFLSK 60

QY 166 NLHONLIRKPKGDVISVEKTVKCLDITFKHTDEEFLKQASSOKPAWKDGSTATCVLAV 225
Db 61 NLPEILABELIKDK--DEDEDVEDALRKAFRTDEEILEELESLEDQ--RSGTTAVVALIR 117

QY 226 DNILYIANLGSRAILCRYNESQKHAALSLSKEHNPTQYEEWRIRIQKAGNVRDGVILG 285
Db 118 GNKLYVANVGSRAVLCRNGK-----AVQLTEDEKPSNEDEDERIRIEAGGFVSNGRVNG 171

QY 286 VLEYSRSTGQYKRCGVTSVDPDPRCOLTPNDPFIILLACDGLFKVTPPEANFNILSCL 345
Db 172 VLASRAUGD--FFLKPYVIAEPDVTVVTELTBKDFLIASDGLMDVLSNQEVVDIV---- 226

QY 346 EDEKIQTREGKSAADARYEAACNLKAVKAVQSGADNVVMV 388
Db 227 -----RHLKSGGQEAAKLIDLAIRGSKDNITVVVV 260

RESULT 7
US-10-170-789-35
/ Sequence 35, Application US/10170789
/ Publication No. US20030180930A1
/ GENERAL INFORMATION:
/ APPLICANT: Rachel E. Meyers
/ APPLICANT: Olandt, Peter J.
/ APPLICANT: Kapeller-Libermann, Rosana
/ APPLICANT: Curtis, Rory A. J.
/ APPLICANT: Williamson, Mark
/ APPLICANT: Weich, Nadine
/ TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASE, PHOSPHATASE,
/ FILE OF INVENTION: AND PROTEASE FAMILY MEMBERS AND USES THEREOF
/ FILE REFERENCE: 10448-191001
/ CURRENT APPLICATION NUMBER: US/10/170,789
/ CURRENT FILING DATE: 2002-06-13
/ PRIOR APPLICATION NUMBER: US 09/797,039
/ PRIOR FILING DATE: 2001-02-28
/ PRIOR APPLICATION NUMBER: PCT/US01/06525
/ PRIOR FILING DATE: 2001-02-28
/ PRIOR APPLICATION NUMBER: US 60/186,061
/ PRIOR FILING DATE: 2000-02-29
/ PRIOR APPLICATION NUMBER: US 09/882,166
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: PCT/US01/19269
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: US 60/212,078
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: US 09/934,406
/ PRIOR FILING DATE: 2001-08-21
/ PRIOR APPLICATION NUMBER: PCT/US01/26052
/ PRIOR FILING DATE: 2001-08-21
/ PRIOR APPLICATION NUMBER: US 60/226,740
/ PRIOR FILING DATE: 2000-08-21
/ PRIOR APPLICATION NUMBER: US 09/861,801

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/ PRIOR FILING DATE: 2001-05-21
/ PRIOR APPLICATION NUMBER: PCT/US01/16549
/ PRIOR FILING DATE: 2001-05-21
/ PRIOR APPLICATION NUMBER: US 60/205,508
/ PRIOR FILING DATE: 2000-05-19
/ PRIOR APPLICATION NUMBER: US 09/801,267
/ PRIOR FILING DATE: 2001-03-06
/ PRIOR APPLICATION NUMBER: PCT/US01/07138
/ PRIOR FILING DATE: 2001-03-05
/ PRIOR APPLICATION NUMBER: US 60/187,454
/ PRIOR FILING DATE: 2000-03-07
/ PRIOR APPLICATION NUMBER: US 09/829,671
/ PRIOR FILING DATE: 2001-04-10
/ PRIOR APPLICATION NUMBER: PCT/US01/40483
/ PRIOR FILING DATE: 2001-04-11
/ PRIOR APPLICATION NUMBER: US 60/197,508
/ PRIOR FILING DATE: 2000-04-18
/ PRIOR APPLICATION NUMBER: US 09/961,721
/ PRIOR FILING DATE: 2001-09-24
/ PRIOR APPLICATION NUMBER: PCT/US01/29904
/ PRIOR FILING DATE: 2001-09-24
/ PRIOR APPLICATION NUMBER: US 60/235,023
/ PRIOR FILING DATE: 2000-09-25
/ PRIOR APPLICATION NUMBER: US 10/045,367
/ PRIOR FILING DATE: 2001-11-07
/ PRIOR APPLICATION NUMBER: US 60/246,561
/ PRIOR FILING DATE: 2000-11-07
/ PRIOR APPLICATION NUMBER: US 09/801,275
/ PRIOR FILING DATE: 2001-03-06
/ PRIOR APPLICATION NUMBER: PCT/US01/07074
/ PRIOR FILING DATE: 2001-03-05
/ PRIOR APPLICATION NUMBER: US 60/187,420
/ PRIOR FILING DATE: 2000-03-07
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 35
/ LENGTH: 300
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: consensus sequence
US-10-170-789-35

Query Match          20.9%; Score 421.5; DB 14; Length 300;
Best Local Similarity 36.4%; Pred. No. 5.4e-31;
Matches 114; Conservative 56; Mismatches 86; Indels 57; Gaps 15;

QY 111 VAERGEREMQDAHVILNDITECPSPSSLITRVSYFAVFDGHHGIRASKFAAQNLHQN 170
Db 5 VERMQGRKSMEDAHIALKNLNSSSSGKDSW-----SFFAVFDGHS-QAAKYAGKHLKT 59

QY 171 LI--RKPPKGD-----VISVEKTVKRCLLDTFKHTDEEFLKQASS-----QKPAWKDG 216
Db 60 ILAERKSPFEGDFWEMKJLSDLEDAKESFLEA--DTDEELSAEASAAANKVLTEDLSSG 117

QY 217 STATCVLAVDNILYIANLGSRAILCRYNESQKHAALSLSKEHNPTQYEEWRIRIQKAGG 276
Db 118 STAVVALTRGNKLYVANVGDSEAVLCR--NGNAIKW-AVLTIEDHKPSNEDEDERIEAAGG 175

QY 277 ---NVRDGRVLGVLEVSRSIGDQYK---RCG-----VTSVPDI--RR 311
Db 176 FVSRVSNRVRNGVLAVSRAFGDFELKPGSKLGPBESLEANVEYIKSPQLVTAEPDVTSS 235

QY 312 COLTEN--DRFILLACDGLFKVTPPEAVNFIILSLEDKIQTRCKSKSAADARYEAACNL 370
Db 236 TDLTPDKDFEFLIACDGLMDVYVSDQEVVDIVRSELS-----GNKSAEDPMEAA--EKL 287

QY 371 ANKAVQSGADNV 383
Db 288 VDEIARGSEDNI 300

RESULT 8

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RESULT 10
US-10-424-599-226412
; Sequence 226412, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kowalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

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Query Match      20.0%; Score 403.5; DB 12; Length 252;
Best Local Similarity 37.3%; Pred. No. 2.1e+29;
Matches 104; Conservative 53; Mismatches 85; Indels 37; Gaps 10;

111 VAERKGRREEMQDAHVILNDITTECPPLSLTRVSYFAVFDGHGIGIRASFAAQLHQN 170
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Ddb      5 VSRVQGFKEFWEDAHIAKKNLNSGGKDK-----GFAVFDGHGSGQAATAGKHLETK 59
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

171 L-IRK-PPKGDVISVEKTVKRCILDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNI 228
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

; TITLE OF INVENTION: plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 226412
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_4647C.1.pap
US-10-424-599-226412

Query Match 20.0%; Score 403.5; DB 12; Length 338;
Best Local Similarity 39.2%; Pred. No. 3.2e-29;
Matches 112; Conservative 44; Mismatches 83; Indels 47; Gaps 13;
QY 109 GYAEKGEREMQDAH-VILNDITECRPPSSLLITRVSVFAVDFGHHGIRASKFAAQN 167
DB 81 GY-ASSPKRSSMGDFYETRIDGVGEV-----VGLFGVDFGHHGIRAAEYVKQNL 130
QY 168 HONLRKPKGDVISVEKTVKRCLLDTFKHTDEBFLKQASSQKPAWKD-GSTATCVLAVD 226
DB 131 FSNLI-SHPK--FIS---DTSAADAVNHTDSFLKSENNQN---RDAGSTASTAILVG 181
QY 227 NILYIANLGDRAILCRYNEESQKHAALSUSKEHNPTQYERMRIOKAGNVR---DGRV 283
DB 182 DRLLVANVGDSRAVICRGN-----AIAVSRDHKPDQTDERRIEDAGGFVWAGTWVR 235
QY 284 LGVLEVSRSIGDQYKRCGVTSVPDIRCOLTPNDRIILLACDGLFKVFTPEEAVNFILS 343
DB 236 GGVLAVSRAFGDRLKQY-VVADPEIQEIKVDSLEFLILASDGLWDVWSNEEAVAMI-- 292
QY 344 CLEDEKIQTREGKSAADARYEAACNRLANKAVQSGADNVTVMVVR 389
DB 293 -----KPIEDA--EAAKRLMQEAYQSGADNITCVVVR 324

RESULT 11
US-10-424-599-219869
; Sequence 219869, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 219869
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_4056C.1.pap
US-10-424-599-219869

Query Match 19.8%; Score 399.5; DB 12; Length 314;
Best Local Similarity 39.2%; Pred. No. 6.8e-29;
Matches 112; Conservative 42; Mismatches 85; Indels 47; Gaps 13;
QY 109 GYAEKGEREMQDAH-VILNDITECRPPSSLLITRVSVFAVDFGHHGIRASKFAAQN 167
DB 36 GY-ASSPKRSSMGDFYETRIDGVGEV-----VGLFGVDFGHHGIRAAEYVKQNL 85
QY 168 HONLRKPKGDVISVEKTVKRCLLDTFKHTDEBFLKQASSQKPAWKD-GSTATCVLAVD 226
DB 86 FSNLI-SHPK--FIS---DTSAITDAYNHTDSLLKSENNHN---RDAGSTASTAILVG 136

QY 227 NILYIANLGDRAILCRYNEESQKHAALSUSKEHNPTQYERMRIOKAGNVR---DGRV 283
DB 137 DRLLVANVGDSRAVICRGN-----AIAVSRDHKPDQTDERRIEDAGGFVWAGTWVR 190
QY 284 LGVLEVSRSIGDQYKRCGVTSVPDIRCOLTPNDRIILLACDGLFKVFTPEEAVNFILS 343
DB 191 GGVLAVSRAFGDRLKQY-VVADPEIQEIKVDSLEFLILASDGLWDVWSNEEAVAMI-- 247
QY 344 CLEDEKIQTREGKSAADARYEAACNRLANKAVQSGADNVTVMVVR 389
DB 248 -----KPIEDA--EAAKRLMQEAYQSGADNITCVVVR 279
RESULT 12
US-10-424-599-219880
; Sequence 219880, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 219880
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_4057C.1.pap
US-10-424-599-219880

Query Match 19.7%; Score 397.5; DB 12; Length 312;
Best Local Similarity 39.3%; Pred. No. 1e-28;
Matches 112; Conservative 41; Mismatches 87; Indels 45; Gaps 12;
QY 109 GYAEKGEREMQDAH-VILNDITECRPPSSLLITRVSVFAVDFGHHGIRASKFAAQN 168
DB 36 GY-ASSPKRSSMGDFYETRIDGVGEV-----BIVGLFGVDFGHHGIRAAEYVKQNL 86
QY 169 HONLRKPKGDVISVEKTVKRCLLDTFKHTDEBFLKQASSQKPAWKD-GSTATCVLAVD 227
DB 87 FSNLI-SHPK--FIS---DTSAITDAYNHTDSLLKSENNHN---RDAGSTASTAILVG 137
QY 228 ILYIANLGDRAILCRYNEESQKHAALSUSKEHNPTQYERMRIOKAGNVR---DGRV 284
DB 138 RLLVANVGDSRAVICRGN-----AIAVSRDHKPDQTDERRIEDAGGFVWAGTWVR 191
QY 285 GVLVSRSIGDQYKRCGVTSVPDIRCOLTPNDRIILLACDGLFKVFTPEEAVNFILS 344
DB 192 GVLVSRAFGDRLKQY-VVADPEIQEIKVDSLEFLILASDGLWDVWSNEEAVAMI--- 247
QY 345 CLEDEKIQTREGKSAADARYEAACNRLANKAVQSGADNVTVMVVR 389
DB 248 -----KPIEDA--EAAKRLMQEAYQSGADNITCVVVR 279
RESULT 13
US-09-860-351-4
; Sequence 4, Application US/09860351
; Patent No. US20020077463A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 16105, A NOVEL PROTEIN HUMAN PHOSPHATASE
; FILE REFERENCE: 38155-20013.00
; CURRENT APPLICATION NUMBER: US/09/860,351
; CURRENT FILING DATE: 2001-05-17

PRIOR APPLICATION NUMBER: US 60/205,260
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 274
TYPE: PR1
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus amino acid
US-09-860-351-4

Query Match 19.6%; Score 395.5; DB 9; Length 274;
Best Local Similarity 36.7%; Pred. No. 1.3e-28;
Matches 106; Conservative 49; Mismatches 79; Indels 55; Gaps 13;

QY 118 REEMQDAHVINDITECRPPSSLIITRVSYFVFDGHHGGRASKFAAQNHLQNLII---RX 174
DB 1 RKSMEDAHIALKNLSSSSGKDSW-----SFFAVFDGHHGGRASKFAAQNHLQNLIIAERKS 56
QY 175 FPKGD-----VISVEKTVKGLDFTFKHTDBEFLKQASS-----QKPAKDGSTATCVL 223
DB 57 FPEGDPWEMKLUDEDALKSFLEA--DTDEELRSASAAANKVLTKEDESSGSTAVVAL 114
QY 224 AVDNILYIANLGDRAILCRYNEESQKHAALSLSKEHNPTQYERMRIOKAGG---NVRD 280
DB 115 IRGNKLYVAVGDSRAVLCR-NGNAIKW-AVLTEDHKPSNEDEREIEAAGGFVSRVSN 172
QY 281 GRVLGVLEVSRIQGGQYK---RCG-----VTSVPDI--RRCQLTPN- 317
DB 173 GRVNGVLAVSRAFGDFELKPGSKLGPESLEANVEYIKSPQLVTAEPDVTSTDLTPDK 232
QY 318 DRFILLACDGLFKVFTPEEAANFILSCLEDEKIQTRGKSAADARYEAA 366
DB 233 DEFLIACDGLWVDSQEVVDIVRSELS-----GNKSAEDPMEAA 274

RESULT 14
US-10-425-114-66152
Sequence 66152, Application US/10425114
Publication No. US20040034889A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 66152
LENGTH: 371
TYPE: PR1
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB4602-009-A7_FLI.pep
US-10-425-114-66152

Query Match 19.2%; Score 388; DB 12; Length 371;
Best Local Similarity 37.0%; Pred. No. 1.1e-27;
Matches 105; Conservative 51; Mismatches 82; Indels 46; Gaps 11;

QY 111 VAERKGEREQDAH-VILNDITECRPPSSLIITRVSYFVFDGHHGGRASKFAAQNHLQ 169
DB 107 VASSPGKASMEDFFEARIDVDGE-----KVGMFVYDGHGGVRAAEYVKQHLFS 157
QY 170 NLIRKFPKGDVISVEKTVKRCLLDFTFKHTDBEFLKQASSQKPAWKD--GSTATCVLVDNI 228
DB 158 NLI-KHPK-----FITDTKAAIAETYNRTDSEFLKADSTQT---RDAGSTASTAIIVGDR 208

PRIOR APPLICATION NUMBER: US 60/205,260
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 274
TYPE: PR1
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus amino acid
US-09-860-351-4

Query Match 19.6%; Score 395.5; DB 9; Length 274;
Best Local Similarity 36.7%; Pred. No. 1.3e-28;
Matches 106; Conservative 49; Mismatches 79; Indels 55; Gaps 13;

QY 118 REEMQDAHVINDITECRPPSSLIITRVSYFVFDGHHGGRASKFAAQNHLQNLII---RX 174
DB 1 RKSMEDAHIALKNLSSSSGKDSW-----SFFAVFDGHHGGRASKFAAQNHLQNLIIAERKS 56
QY 175 FPKGD-----VISVEKTVKGLDFTFKHTDBEFLKQASS-----QKPAKDGSTATCVL 223
DB 57 FPEGDPWEMKLUDEDALKSFLEA--DTDEELRSASAAANKVLTKEDESSGSTAVVAL 114
QY 224 AVDNILYIANLGDRAILCRYNEESQKHAALSLSKEHNPTQYERMRIOKAGG---NVRD 280
DB 115 IRGNKLYVAVGDSRAVLCR-NGNAIKW-AVLTEDHKPSNEDEREIEAAGGFVSRVSN 172
QY 281 GRVLGVLEVSRIQGGQYK---RCG-----VTSVPDI--RRCQLTPN- 317
DB 173 GRVNGVLAVSRAFGDFELKPGSKLGPESLEANVEYIKSPQLVTAEPDVTSTDLTPDK 232
QY 318 DRFILLACDGLFKVFTPEEAANFILSCLEDEKIQTRGKSAADARYEAA 366
DB 233 DEFLIACDGLWVDSQEVVDIVRSELS-----GNKSAEDPMEAA 274

RESULT 14
US-10-425-114-66152
Sequence 66152, Application US/10425114
Publication No. US20040034889A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 66152
LENGTH: 371
TYPE: PR1
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB4602-009-A7_FLI.pep
US-10-425-114-66152

Query Match 19.2%; Score 388; DB 12; Length 371;
Best Local Similarity 37.0%; Pred. No. 1.1e-27;
Matches 105; Conservative 51; Mismatches 82; Indels 46; Gaps 11;

QY 111 VAERKGEREQDAH-VILNDITECRPPSSLIITRVSYFVFDGHHGGRASKFAAQNHLQ 169
DB 107 VASSPGKASMEDFFEARIDVDGE-----KVGMFVYDGHGGVRAAEYVKQHLFS 157
QY 170 NLIRKFPKGDVISVEKTVKRCLLDFTFKHTDBEFLKQASSQKPAWKD--GSTATCVLVDNI 228
DB 158 NLI-KHPK-----FITDTKAAIAETYNRTDSEFLKADSTQT---RDAGSTASTAIIVGDR 208

PRIOR APPLICATION NUMBER: US 60/205,260
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 274
TYPE: PR1
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus amino acid
US-09-860-351-4

Query Match 19.6%; Score 395.5; DB 9; Length 274;
Best Local Similarity 36.7%; Pred. No. 1.3e-28;
Matches 106; Conservative 49; Mismatches 79; Indels 55; Gaps 13;

QY 118 REEMQDAHVINDITECRPPSSLIITRVSYFVFDGHHGGRASKFAAQNHLQNLII---RX 174
DB 1 RKSMEDAHIALKNLSSSSGKDSW-----SFFAVFDGHHGGRASKFAAQNHLQNLIIAERKS 56
QY 175 FPKGD-----VISVEKTVKGLDFTFKHTDBEFLKQASS-----QKPAKDGSTATCVL 223
DB 57 FPEGDPWEMKLUDEDALKSFLEA--DTDEELRSASAAANKVLTKEDESSGSTAVVAL 114
QY 224 AVDNILYIANLGDRAILCRYNEESQKHAALSLSKEHNPTQYERMRIOKAGG---NVRD 280
DB 115 IRGNKLYVAVGDSRAVLCR-NGNAIKW-AVLTEDHKPSNEDEREIEAAGGFVSRVSN 172
QY 281 GRVLGVLEVSRIQGGQYK---RCG-----VTSVPDI--RRCQLTPN- 317
DB 173 GRVNGVLAVSRAFGDFELKPGSKLGPESLEANVEYIKSPQLVTAEPDVTSTDLTPDK 232
QY 318 DRFILLACDGLFKVFTPEEAANFILSCLEDEKIQTRGKSAADARYEAA 366
DB 233 DEFLIACDGLWVDSQEVVDIVRSELS-----GNKSAEDPMEAA 274

RESULT 14
US-10-425-114-66152
Sequence 66152, Application US/10425114
Publication No. US20040034889A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 66152
LENGTH: 371
TYPE: PR1
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB4602-009-A7_FLI.pep
US-10-425-114-66152

Query Match 19.2%; Score 388; DB 12; Length 371;
Best Local Similarity 37.0%; Pred. No. 1.1e-27;
Matches 105; Conservative 51; Mismatches 82; Indels 46; Gaps 11;

QY 111 VAERKGEREQDAH-VILNDITECRPPSSLIITRVSYFVFDGHHGGRASKFAAQNHLQ 169
DB 107 VASSPGKASMEDFFEARIDVDGE-----KVGMFVYDGHGGVRAAEYVKQHLFS 157
QY 170 NLIRKFPKGDVISVEKTVKRCLLDFTFKHTDBEFLKQASSQKPAWKD--GSTATCVLVDNI 228
DB 158 NLI-KHPK-----FITDTKAAIAETYNRTDSEFLKADSTQT---RDAGSTASTAIIVGDR 208

PRIOR APPLICATION NUMBER: US 60/205,260
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 274
TYPE: PR1
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus amino acid
US-09-860-351-4

Query Match 19.6%; Score 395.5; DB 9; Length 274;
Best Local Similarity 36.7%; Pred. No. 1.3e-28;
Matches 106; Conservative 49; Mismatches 79; Indels 55; Gaps 13;

QY 118 REEMQDAHVINDITECRPPSSLIITRVSYFVFDGHHGGRASKFAAQNHLQNLII---RX 174
DB 1 RKSMEDAHIALKNLSSSSGKDSW-----SFFAVFDGHHGGRASKFAAQNHLQNLIIAERKS 56
QY 175 FPKGD-----VISVEKTVKGLDFTFKHTDBEFLKQASS-----QKPAKDGSTATCVL 223
DB 57 FPEGDPWEMKLUDEDALKSFLEA--DTDEELRSASAAANKVLTKEDESSGSTAVVAL 114
QY 224 AVDNILYIANLGDRAILCRYNEESQKHAALSLSKEHNPTQYERMRIOKAGG---NVRD 280
DB 115 IRGNKLYVAVGDSRAVLCR-NGNAIKW-AVLTEDHKPSNEDEREIEAAGGFVSRVSN 172
QY 281 GRVLGVLEVSRIQGGQYK---RCG-----VTSVPDI--RRCQLTPN- 317
DB 173 GRVNGVLAVSRAFGDFELKPGSKLGPESLEANVEYIKSPQLVTAEPDVTSTDLTPDK 232
QY 318 DRFILLACDGLFKVFTPEEAANFILSCLEDEKIQTRGKSAADARYEAA 366
DB 233 DEFLIACDGLWVDSQEVVDIVRSELS-----GNKSAEDPMEAA 274

RESULT 14
US-10-425-114-66152
Sequence 66152, Application US/10425114
Publication No. US20040034889A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 66152
LENGTH: 371
TYPE: PR1
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB4602-009-A7_FLI.pep
US-10-425-114-66152

Query Match 19.2%; Score 388; DB 12; Length 371;
Best Local Similarity 37.0%; Pred. No. 1.1e-27;
Matches 105; Conservative 51; Mismatches 82; Indels 46; Gaps 11;

QY 111 VAERKGEREQDAH-VILNDITECRPPSSLIITRVSYFVFDGHHGGRASKFAAQNHLQ 169
DB 107 VASSPGKASMEDFFEARIDVDGE-----KVGMFVYDGHGGVRAAEYVKQHLFS 157
QY 170 NLIRKFPKGDVISVEKTVKRCLLDFTFKHTDBEFLKQASSQKPAWKD--GSTATCVLVDNI 228
DB 158 NLI-KHPK-----FITDTKAAIAETYNRTDSEFLKADSTQT---RDAGSTASTAIIVGDR 208

OM protein - protein search, using sw model

Run on: April 12, 2004, 09:05:12 ; Search time 23 Seconds
(without alignments)
879.886 Million cell updates/sec

Title: US-09-935-124A-2
Perfect score: 2018
Sequence: 1 MDLFGDLPERSPRPAAGK.....KAVORGADNVTVMVWVIGH 392

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A COMB.psp:*
2: /cgn2_6/ptodata/2/iaa/5B COMB.psp:*
3: /cgn2_6/ptodata/2/iaa/6A COMB.psp:*
4: /cgn2_6/ptodata/2/iaa/6B COMB.psp:*
5: /cgn2_6/ptodata/2/iaa/FACTUS COMB.psp:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.psp:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2018	100.0	392	3	US-09-013-881-2
2	2018	100.0	392	4	US-09-613-473-2
3	340	15.8	306	2	US-08-822-701-8
4	340	15.8	306	3	US-08-935-855-8
5	326	15.2	390	4	US-09-206-646-4
6	320.5	15.9	309	2	US-08-822-701-7
7	320.5	15.9	309	3	US-08-935-855-7
8	319	15.8	390	2	US-08-873-093-3
9	319	15.8	390	4	US-09-206-646-3
10	317.5	15.7	281	2	US-08-822-701-9
11	317.5	15.7	281	3	US-08-935-855-9
12	314	15.6	372	4	US-09-973-963-4
13	313	15.5	478	2	US-08-873-093-1
14	313	15.5	478	2	US-08-873-093-4
15	313	15.5	479	4	US-09-206-646-1
16	312	15.5	387	4	US-09-461-325-178
17	312	15.5	387	4	US-10-012-542-178
18	271.5	13.5	314	3	US-08-822-701-10
19	271.5	13.5	314	3	US-08-935-855-10
20	269.5	13.4	392	2	US-08-822-701-2
21	269.5	13.4	392	3	US-08-935-855-2
22	269.5	13.4	542	3	US-08-935-855-22
23	255.5	12.7	546	3	US-08-935-855-20
24	178	8.8	504	2	US-08-752-891-2
25	178	8.8	504	2	US-09-144-178-2
26	178	8.8	504	3	US-09-406-854-2
27	178	8.8	504	4	US-09-529-279-2

Sequence 2, Appli
Sequence 43, Appli
Sequence 43, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 4701, Ap
Sequence 6748, Ap
Sequence 171, App
Sequence 4777, Ap
Sequence 22696, A
Sequence 10, Appl
Sequence 10, Appl
Sequence 13, Appl
Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-013-881-2
; Sequence 2, Application US/09013881
; Patent No. 6132964
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Puri
; TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/013,881
; FILING DATE: HEREMITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BILLINGS, LUCY J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0470 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 392 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KIDNOT02
; CLONE: 195647
US-09-013-881-2

Query Match 100.0%; Score 2018; DB 3; Length 392;
Best Local Similarity 100.0%; Pred. No. 1.3e-200;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPRAAGKEAQKGPLLFDLPASSTDSGGPGLLFDLPASSGDSG 60
Db 1 MDLFGDLPEPERSPPRAAGKEAQKGPLLFDLPASSTDSGGPGLLFDLPASSGDSG 60

QY 61 SLATISQWKTEGKAKRTSBEKNGSEELVEKVKCKASSVIFGLKGVVAERKGEREE 120
Db 61 SLATISQWKTEGKAKRTSBEKNGSEELVEKVKCKASSVIFGLKGVVAERKGEREE 120

QY 121 MODAHVILNDITECRPPSSLIITRVSFAVFDGHHGIRASKFAAQNHLQNLIRKFPKGDV 180
Db 121 MODAHVILNDITECRPPSSLIITRVSFAVFDGHHGIRASKFAAQNHLQNLIRKFPKGDV 180

QY 181 ISVEKTVKRCCLLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDSPAI 240
Db 181 ISVEKTVKRCCLLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDSPAI 240

QY 241 LCRNEESQKHAALSLSKEHNPTQYEBMRIOKAGNVDRGRVGLVLEVSRSIGDQYKR 300
Db 241 LCRNEESQKHAALSLSKEHNPTQYEBMRIOKAGNVDRGRVGLVLEVSRSIGDQYKR 300

QY 301 CGVTSVPDIRRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQITREGKSAAD 360
Db 301 CGVTSVPDIRRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQITREGKSAAD 360

QY 361 ARYEACNRLANKAVQSGADNVTVMVVRIGH 392
Db 361 ARYEACNRLANKAVQSGADNVTVMVVRIGH 392

RESULT 2
US-09-612-473-2
; Sequence 2, Application US/09612473
; Patent No. 6518029
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
; FILE REFERENCE: PF-0470-1 CIP
; CURRENT APPLICATION NUMBER: US/09/612,473
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/013,881
; PRIOR FILING DATE: 1998-02-06
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6518029 195647
US-09-612-473-2

Query Match 100.0%; Score 2018; DB 4; Length 392;
Best Local Similarity 100.0%; Pred. No. 1.3e-200;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPRAAGKEAQKGPLLFDLPASSTDSGGPGLLFDLPASSGDSG 60
Db 1 MDLFGDLPEPERSPPRAAGKEAQKGPLLFDLPASSTDSGGPGLLFDLPASSGDSG 60

QY 61 SLATISQWKTEGKAKRTSBEKNGSEELVEKVKCKASSVIFGLKGVVAERKGEREE 120
Db 61 SLATISQWKTEGKAKRTSBEKNGSEELVEKVKCKASSVIFGLKGVVAERKGEREE 120

QY 121 MODAHVILNDITECRPPSSLIITRVSFAVFDGHHGIRASKFAAQNHLQNLIRKFPKGDV 180
Db 121 MODAHVILNDITECRPPSSLIITRVSFAVFDGHHGIRASKFAAQNHLQNLIRKFPKGDV 180

QY 181 ISVEKTVKRCCLLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDSPAI 240
Db 181 ISVEKTVKRCCLLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDSPAI 240

QY 241 LCRNEESQKHAALSLSKEHNPTQYEBMRIOKAGNVDRGRVGLVLEVSRSIGDQYKR 300
Db 241 LCRNEESQKHAALSLSKEHNPTQYEBMRIOKAGNVDRGRVGLVLEVSRSIGDQYKR 300

QY 301 CGVTSVPDIRRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQITREGKSAAD 360
Db 301 CGVTSVPDIRRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQITREGKSAAD 360

QY 361 ARYEACNRLANKAVQSGADNVTVMVVRIGH 392
Db 361 ARYEACNRLANKAVQSGADNVTVMVVRIGH 392

RESULT 3
US-08-822-701-8
; Sequence 8, Application US/08822701
; Patent No. 5976853
; GENERAL INFORMATION:
; APPLICANT: Guthridge, Mark
; APPLICANT: Basilico, Claudio
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,701
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-002 N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 306 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Rattus
US-08-822-701-8

Query Match 16.8%; Score 340; DB 2; Length 306;
Best Local Similarity 33.7%; Pred. No. 9.6e-27;
Matches 101; Conservative 47; Mismatches 104; Indels 48; Gaps 12;

QY	106	GLKGYAERKGEREEMQDAHVILNDITECRPPSSLITRVSYFAVFDGHGIRASKFAAQ	165
Db	21	GLRYGLSSMQGWRVEMEDAHTAVIGL-----PSGLET-WSFFAVYDGHAGSQVAKYCC	73
QY	166	NLHQNLRKFP-KGD--VISVEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKDGSTATCV	222
Db	74	HLDDHITNNQDPKGSAGAPSVN-NGKGI RTGFLIDEHMRVMSKKHKGADRSGSTAVGV	132
QY	223	LAVDNLIYANLGDRAILCRYNEESQKHAALSLSKEHNPTQYERMRIOKAGGNVRDGR	282
Db	133	LISPHQTYFINGDSRGLLCLR-----NRKVHFFTDQHKPSNPLEKERIQNAGGSVMQIR	186
QY	283	VLGVLEVSRSIGDGOYKRC-----GVT-----SVPDIRCQLTNPDRFILLACDGLFK	330
Db	187	VNGSLAVSRALGDPDYK-CVHGKGFTQELVSPPEVHDIERSE--EDDQFILLACDGIWD	243
QY	331	VFTPEAVNFILSCLE--DEKIQTRGKSAADARYEACNRLANKAVQSGADNVTVMVY	388
Db	244	VMGNEELCDFVRSRLEVTD-----LEKVCNEVVDTCLYKGSRDNMNVILI	289
RESULT 4			
US-08-935-855-8			
; Sequence 8, Application US/08935855			
; Patent No. 6066485			
; GENERAL INFORMATION:			
; APPLICANT: Guthridge, Mark			
; APPLICANT: Basilio, Claudio			
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE			
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13			
; NUMBER OF SEQUENCES: 22			
; CORRESPONDENCE ADDRESS:			
; ADDRESS: David A. Jackson, Esq.			
; STREET: 411 Hackensack Ave, Continental Plaza, 4th			
; CITY: Hackensack			
; STATE: New Jersey			
; COUNTRY: USA			
; ZIP: 07601			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent in Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/935,855			
; FILING DATE:			
; CLASSIFICATION: 435			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Jackson Esq., David A.			
; REGISTRATION NUMBER: 26,742			
; REFERENCE/DOCKET NUMBER: 1049-1-002 CIP			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 201-487-5800			
; TELEFAX: 201-343-1684			
; INFORMATION FOR SEQ ID NO: 8:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 306 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
; HYPOTHETICAL: NO			
; FRAGMENT TYPE:			
; ORIGINAL SOURCE:			
; ORGANISM: Rattus			
US-08-935-855-8			
Query Match 16.8%; Score 340; DB 3; Length 306;			
Best Local Similarity 33.7%; Pred. No. 9,6e-27;			
Matches 101; Conservative 47; Mismatches 104; Indels 48; Gaps 12;			
QY	106	GLKGYAERKGEREEMQDAHVILNDITECRPPSSLITRVSYFAVFDGHGIRASKFAAQ	165

Db	21	GLRYGLSSMQGWRVEMEDAHTAVIGL-----PSGLET-WSFFAVYDGHAGSQVAKYCC	73
QY	166	NLHQNLRKFP-KGD--VISVEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKDGSTATCV	222
Db	74	HLDDHITNNQDPKGSAGAPSVN-NGKGI RTGFLIDEHMRVMSKKHKGADRSGSTAVGV	132
QY	223	LAVDNLIYANLGDRAILCRYNEESQKHAALSLSKEHNPTQYERMRIOKAGGNVRDGR	282
Db	133	LISPHQTYFINGDSRGLLCLR-----NRKVHFFTDQHKPSNPLEKERIQNAGGSVMQIR	186
QY	283	VLGVLEVSRSIGDGOYKRC-----GVT-----SVPDIRCQLTNPDRFILLACDGLFK	330
Db	187	VNGSLAVSRALGDPDYK-CVHGKGFTQELVSPPEVHDIERSE--EDDQFILLACDGIWD	243
QY	331	VFTPEAVNFILSCLE--DEKIQTRGKSAADARYEACNRLANKAVQSGADNVTVMVY	388
Db	244	VMGNEELCDFVRSRLEVTD-----LEKVCNEVVDTCLYKGSRDNMNVILI	289
RESULT 5			
US-09-206-646-4			
; Sequence 4, Application US/09206646			
; Patent No. 6436637			
; GENERAL INFORMATION:			
; APPLICANT: Bandman, Olga			
; APPLICANT: Goli, Surya K.			
; APPLICANT: Lal, Preeti G.			
; APPLICANT: Corley, Neil C.			
; APPLICANT: Zhang, Hong			
; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE			
; FILE REFERENCE: PF-0319-1 DIV			
; CURRENT APPLICATION NUMBER: US/09/206,646			
; CURRENT FILING DATE: 2001-12-07			
; NUMBER OF SEQ ID NOS: 4			
; SOFTWARE: PERL Program			
; SEQ ID NO 4			
; LENGTH: 390			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc feature			
; OTHER INFORMATION: ID No. 6436637 g452526			
US-09-206-646-4			
Query Match 16.2%; Score 326; DB 4; Length 390;			
Best Local Similarity 30.0%; Pred. No. 4e-25;			
Matches 98; Conservative 52; Mismatches 121; Indels 56; Gaps 10;			
QY	78	KRTSEEEKNGSEELVEKKVKCKASSVIFGLKGYAERKGEREEMQDAHVILNDITECRP	137
Db	7	KPKTEKHNAHGAGN-----GLRYGLSSMQGWRVEMEDAHTAVVGI-----	46
QY	138	PSLITRVSYFAVFDGHGIRASKFAAQNLHQN-----IRKFPK-GDVI--SVEKTVKR	189
Db	47	PHGL-DNWSFFAVYDGHAGSRVANYCSTHLLSHITTNEEDFRAADKSGSALEPSVE-SVKT	104
QY	190	CLLDTFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNLIYANLGDSEAILCRYNEESQ	249
Db	105	GIRTGFLKIDEMYRNFSDLRNGMDRSGSTAVGVMSPTHYFINGDSSAVLCRNGQ----	161
QY	250	KHAALSLSKEHNPTQYERMRIOKAGGNVRDQRLVGLVEVSRSIGDGOYKRCG-----	302
Db	162	---VCFSTQDHKEFCNPVEKERIQNAGGSVMQIRVNGSLAVSRALGDYDKVDGKGP	218
QY	303	-VTSVPDIRCQLTNPDRFILLACDGLFKVFTPEAVNFILSCLEDEKIQTRGKSAADA	361
Db	219	LVSPEPEVVEIVRABEDFVWLACDGIWDVMSNEELCEPVKSRLE-----VSD	266
QY	362	RYEACNRLANKAVQSGADNVTVMVY	388
Db	267	DLENVCNVVVDTCCLKHKS RDNMNVILV	293

Db 215 TEQLVSPPEVVEIYRAEDEFVWLACDGIWDMVMSNEELCFVKSRLB----- 262

QY 359 ADARAEACNRLANKAVORGSDNVTVMV 388

Db 263 VSDLENCNVWVDTCLHKGRDNNMSIVLV 292

RESULT 8

US-08-873-093-3

Sequence 3, Application US/08873093

Patent No. 5853997

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Goli, Surya K.

APPLICANT: Lal, Preeti

APPLICANT: Corley, Neil C.

APPLICANT: Zhang, Hong

TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/873,093

FILING DATE: Filed Herewith

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0319 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 390 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: 1247927

US-08-873-093-3

Query Match 15.8%; Score 319; DB 2; Length 390;

Best Local Similarity 29.4%; Pred. No. 2.1e-24;

Matches 96; Conservative 51; Mismatches 124; Indels 56; Gaps 9;

QY 78 KEKTSSEKNGSEELVEKVKCKASSVIFGLKGYVAERKGEREEMQDAHVILNDITECRP 137

Db 7 KPKTEKNAHAGN-----GLRYGLSSMOGWVEMEDAHTAVVGI----- 46

QY 138 PSSLIITRVSYFAVFDGHGIRASKFAAQNHLN-----IRKFPKGDVI-----SVEKTVKR 189

Db 47 PHGL-EDWSFFAVYDGHAGSRVANYCSTHLEHITTNEDFRAADKSGFALEPSVE-NVKT 104

QY 190 CLLDTEFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLGDSRAILCRYNESQ 249

Db 105 GIRTGFLKIDEMRNFSDLRNGMDRSGSTAVGVMISPTHYIFINCGDSRAVLCRNGQ--- 161

QY 250 KHAALSLSKEHNPTQYEERMRIQKAGNVDRGVLEVSRSIGDGQYKRCG----- 302

Db 162 ---VCFSTQDHPKPCNPMEKERIQNAGGSVMIQKVNGSLAVSRALGDIYKCVDKGKPTQ 218

QY 303 -VTSVPDIERCQLTPNDRIFILLACDGLFKVFTPEEAVNFIILSCLEDEKIQTRGKSAADA 361

Db 219 LVSPEPEVVEIYRAEDEFVWLACDGIWDMVMSNEELCFVKSRLB-----VSD 266

Query Match 15.8%; Score 319; DB 2; Length 390;

Best Local Similarity 29.4%; Pred. No. 2.1e-24;

Matches 96; Conservative 51; Mismatches 124; Indels 56; Gaps 9;

QY 78 KEKTSSEKNGSEELVEKVKCKASSVIFGLKGYVAERKGEREEMQDAHVILNDITECRP 137

Db 7 KPKTEKNAHAGN-----GLRYGLSSMOGWVEMEDAHTAVVGI----- 46

QY 138 PSSLIITRVSYFAVFDGHGIRASKFAAQNHLN-----IRKFPKGDVI-----SVEKTVKR 189

Db 47 PHGL-EDWSFFAVYDGHAGSRVANYCSTHLEHITTNEDFRAADKSGFALEPSVE-NVKT 104

QY 190 CLLDTEFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLGDSRAILCRYNESQ 249

Db 105 GIRTGFLKIDEMRNFSDLRNGMDRSGSTAVGVMISPTHYIFINCGDSRAVLCRNGQ--- 161

QY 250 KHAALSLSKEHNPTQYEERMRIQKAGNVDRGVLEVSRSIGDGQYKRCG----- 302

Db 162 ---VCFSTQDHPKPCNPMEKERIQNAGGSVMIQKVNGSLAVSRALGDIYKCVDKGKPTQ 218

QY 303 -VTSVPDIERCQLTPNDRIFILLACDGLFKVFTPEEAVNFIILSCLEDEKIQTRGKSAADA 361

Db 219 LVSPEPEVVEIYRAEDEFVWLACDGIWDMVMSNEELCFVKSRLB-----VSD 266

QY 362 RYEAACNRLANKAVORGSDNVTVMV 388

Db 267 DLENCNVWVDTCLHKGRDNNMSIVLV 293

RESULT 9

US-09-206-646-3

Sequence 3, Application US/09206646

Patent No. 6436637

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Goli, Surya K.

APPLICANT: Lal, Preeti G.

APPLICANT: Corley, Neil C.

APPLICANT: Zhang, Hong

TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE

FILE REFERENCE: PF-0319-1 DIV

CURRENT APPLICATION NUMBER: US/09/206,646

CURRENT FILING DATE: 2001-12-07

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PERL Program

SEQ ID NO 3

LENGTH: 390

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: ID No. 6436637 g247927

US-09-206-646-3

Query Match 15.8%; Score 319; DB 4; Length 390;

Best Local Similarity 29.4%; Pred. No. 2.1e-24;

Matches 96; Conservative 51; Mismatches 124; Indels 56; Gaps 9;

QY 78 KRTSEEEKNGSEELVEKVKCKASSVIFGLKGYVAERKGEREEMQDAHVILNDITECRP 137

Db 7 KPKTEKNAHAGN-----GLRYGLSSMOGWVEMEDAHTAVVGI----- 46

QY 138 PSSLIITRVSYFAVFDGHGIRASKFAAQNHLN-----IRKFPKGDVI-----SVEKTVKR 189

Db 47 PHGL-EDWSFFAVYDGHAGSRVANYCSTHLEHITTNEDFRAADKSGFALEPSVE-NVKT 104

QY 190 CLLDTEFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLGDSRAILCRYNESQ 249

Db 105 GIRTGFLKIDEMRNFSDLRNGMDRSGSTAVGVMISPTHYIFINCGDSRAVLCRNGQ--- 161

QY 250 KHAALSLSKEHNPTQYEERMRIQKAGNVDRGVLEVSRSIGDGQYKRCG----- 302

Db 162 ---VCFSTQDHPKPCNPMEKERIQNAGGSVMIQKVNGSLAVSRALGDIYKCVDKGKPTQ 218

QY 303 -VTSVPDIERCQLTPNDRIFILLACDGLFKVFTPEEAVNFIILSCLEDEKIQTRGKSAADA 361

Db 219 LVSPEPEVVEIYRAEDEFVWLACDGIWDMVMSNEELCFVKSRLB-----VSD 266

QY 362 RYEAACNRLANKAVORGSDNVTVMV 388

Db 267 DLENCNVWVDTCLHKGRDNNMSIVLV 293

RESULT 10

US-06-822-701-9

Sequence 9, Application US/08822701

Patent No. 5976853

GENERAL INFORMATION:

APPLICANT: Guthridge, Mark

APPLICANT: Basilio, Claudio

TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE

TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 STREET: Floor
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/822,701
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 1049-1-002 N
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 281 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 ORGANISM: Saccharomyces cerevisiae
 US-08-822-701-9

Query Match 15.7%; Score 317.5; DB 2; Length 281;

Best Local Similarity 31.4%; Pred. No. 1.8e-24;
Matches 95; Conservative 44; Mismatches 93; Indels 71; Gaps 12;

111	VAERKGE--REEMQDAHVILNDITETCRPPSSLITRV--SYFAVFDGHGGIRASKFAAQN	166
23	VAENKNSKFRRTMEDVHTYVKNFA-----SRLDWGYFAVFDGHAIGIQASKWCGKH	72
167	LH-----QNLIRKFPKGDVISVEKTVKRCLLDTPKHTDEEPLKQASSQKPAWKDGST-ATC	221
73	LHTIIEQNIL-----ADSTRDVRDVLNDSFLAIDEEI-----NTKLVGNSGCTAAVC	119
222	VL-----AVDNI-----LVIANLGDRAILCRYNEESQKHAALSKEHNPTQY	265
120	VLRWELPDSVSDSDMDLAQORKUYTANVGUSRVLVFRNGN-----SIRLTYDHKASOT	173
266	EERMRIQAGGNVRDGRVLGVLEYSRSIGDQYKRCQWTSVPDIRCQLTDPNDRFILLAC	325
174	LEMQRVEQAGGLINKMSRVNGMLATRSLGDKFFDSLUVGS-PTTSVETTSXDKFILLAC	232
326	DGLFKVFTPEEAVNFIILSCLEDEKIQITREGKSAADARYEAACNRLANKAVORGSDNVTV	385
233	DGLWDVIDDQACELIKDIITEPNE-----AAKVLVRYALENGTDTDNVTV	276
386	MTV 388	
277	MTV 279	
	Db	

RESULT 11

US-08-935-855-9

; Sequence 9, Application US/08935855

Patent No. 6066485

GENERAL INFORMATION:

APPLICANT: Guthridge, Mark
 APPLICANT: Basilio, Claudio
 TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
 TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 STREET: Floor
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: /US/08/935,855
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 281 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 ORGANISM: Saccharomyces cerevisiae
 US-08-935-855-9

Query Match 15.7%; Score 317.5; DB 3; Length 281;
Best Local Similarity 31.4%; Pred. No. 1.8e-24;
Matches 95; Conservative 44; Mismatches 93; Indels 71; Gaps 12;

QY	111	VAERKGE--REEMODAHVIINDITEECRPPSSLIITV--SYFAPVDGHCIGTIRASKFAAQN 166
Db	23	VAENKNSKFRRTMEDVHTYVKNFA-----SELDMGYFAPVDGHCIGTIRASKFAAQN 166
QY	167	LH-----QNLIRKPKPGDVISVEKTVKRECLLDTFKHTDEFLKQASSQKPAWKDGT-ATC 221
Db	73	LHTIEQNIL-----ADETRDVRDLNDGFLAIDEI-----NTKLGVNSGCTAAVC 119
QY	222	VL-----AVDNI-----LYTANLGDGRAILCRYNEBSQKFAALSISKEHNPTQY 265
Db	120	VLRLPDSVSDSDMSDLAQORKLYTANVGDSRIVLFRNGN-----SIRLTYDHKASDT 173
QY	266	BERWRIKAGGVNADGRVLGVLEVSRSIGDGYKRCGVTSVPDIRCOLTPNDFRILLAC 325
Db	174	LEMORVEQAGGLIMKSRVNGMLAVTSLGDKFPDSLWGS-PFTTSVEITSEDKFELLILAC 232
QY	326	DGLKVFVTPPEAVNFIILCDESKIOTREKGAADARVEAACNRLANKAVORGSDADNTV 385
Db	233	DGLMDVIDDQACELIKDITEPNE-----AAKVLVRVALENGTTDNTV 276
QY	386	MTV 388
Db	277	MTV 279

RESULT 12

US-09-973-963-4

```

; Sequence 4, Application US/09973963
; Patent No. 6653102
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; TITLE OF INVENTION: Diseases
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,963
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 60/304,775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-973-963-4

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Query Match 15.6%; Score 314; DB 4; Length 372;
Best Local Similarity 27.5%; Pred. No. 6.5e-24;
Matches 110; Conservative 56; Mismatches 120; Indels 114; Gaps 15;

QY	27	LLFDD---LPPASSTDS-----GSGPPLLFDD-----LPPASSDGS	60
Dd	27	: : :	
QY	27	LLODDRVTPTCHSSTSEPRCSRFDPDGSGPATWDFGIWNRIDEPILLPPSI	81
Dd	27	: : :	
QY	61	SLATSISQMVKTECGAKRKTSEEEKNGSBELVEKKVCKKASSVITGLKYVAERKGBEE	120
Dd	61	: : :	
QY	82	-----KYG-----KPPIKSLENVCASQIGKRK-ENED	109
Dd	82	: : :	
QY	121	MODAHVILNDITECRPPSSLI TRVSFAVDGHGGIRASKFAAONLHONLRFPFKGDV	180
Dd	121	: : :	
QY	110	RFD---PAQLTDE-----VLVFAYDGHGGPAAADFCHTFMEKCINDILLPK---	152
Dd	110	: : :	
QY	161	ISVEKTVRCLLDTFKHTDEEFLKQA--SQKPAWKDGTATCVJLAVNI-LYIANLGDS	237
Dd	161	: : :	
QY	153	---EKNLETLTLAFLEIDIKAFSSHARLSADATLTSGTATTALLRDGIELVWASVGDS	209
Dd	153	: : :	
QY	238	RAILCRYNEBSQHAALSLSKEHNPTQYEEMRIQAGG-----NVRDGRVLGVLEVRS	292
Dd	238	: : :	
QY	210	RAILCR-----XGKPMKLTI DHTPEKOEKERIKCGGFVANWSLGP HYNGLAMTRS	263
Dd	210	: : :	
QY	293	IGDGQYKRGCVTSVPDIRRQOL-TPNDRFTLLACDLKFVFTPEEAVNFILSCLEDEKIQ	351
Dd	293	: : :	
QY	264	IGDLLDKTSGVIASEPTRIKLHHADDSELVLT TTDGINFNWNSQICDFVNQCDDPNE-	321
Dd	264	: : :	
QY	352	TREKSAADARYEAACNLANKAVORGSDANTVMVVVRIG	391
Dd	352	: : :	
QY	322	-----AAHAVTEOAI OYGTENSTANVAVVPEG	347
Dd	322	: : :	

RESULT 13
US-08-873-093-1

Sequence 1, Application US/08873093
; Patent No. 5853997

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Zhang, Hong
TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA

COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,093
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0319 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: THPIPL01
CLONE: 13177
US-08-873-093-1

Query Match 15.5%; Score 313; DB 2; Length 478;
Best Local Similarity 28.7%; Pred. No. 1.2e-23;
Matches 94; Conservative 52; Mismatches 125; Indels 56; Gaps 8;

QY	78	KKKTSEEEKXNGSELVEKKVCKASSVIFGLKGVYABRKGERBEMQAHVILNDITBCRP	137
Db	7	KPKTEKHNAHGAGN-----GLRYGLSSMQGWRVEMEDAHTAVGCI-----	46
QY	138	PSLLITRVSYFAVFDCHGIRASKFAAQNHLWLIR-----KPKGQDVISVEKTVKR	189
Db	47	PHGL-EDMSFFAVYDGHAGSRVANYCSTHLEHTTINEDFRAAGKSGSALELSVE-NVKXN	104
QY	190	CLLDFTFKHTDEEFQLQASSQKPAWKDGGSTATCVLAVDNTILYIANLGDRAILCRYNESQ	249
Db	105	GARTGFLKIDETWRNFSDLUNGMDRSGSTAVGVMISPKHIYFINGCDGSRAVLYRNGQ---	161
QY	250	KHAALSLSKEHNPTQVEEEMRIQKAGNVDRGLVGLVSVRSIGGQYKRCG-----	302
Db	162	---VCFSTQDHPKCPREKERIQNAGSGVMIORVNGSLAVSRALGHDYDKVDGKGPTQ	218
QY	303	-VTSVPDIRRCOLTPNDRFILLACDGLFKFVTFEEAVNFILSCLEDEKIQTRREGKSAADA	361
Db	219	LVSPEPEVVEILRAEDEFIILLACDGIWDVMNEELCEYVKSRLE-----VSD	266
QY	362	RYEAAACNRLANKAVQSGADNVTVMVV	388
Db	267	DLENVCNMYDTCILHKGRDNNMSIIV	293

```

RESULT 14
US -08-873-093-4
Sequence 4, Application US/08873093
Patent No. 5953997
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Lal, Preeti
APPLICANT: Corley Neil C.
APPLICANT: Zhang, Hong
TITLE OF INVENTION: NEW PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA: US/08/873,093
APPLICATION NUMBER: US/08/873,093
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0319 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1452526
US-08-873-093-4

Query Match 15.5%; Score 313; DB 2; Length 478;
Best Local Similarity 28.7%; Pred. No. 1.2e-23;
Matches 94; Conservative 52; Mismatches 125; Indels 56; Gaps 8;
QY 78 KRKTSSEKNGSELVEKKVKCKASSVIFGLKGYVAERKGEREEMQDAHVILNDITECRP 137
Db 7 KPKTEKHNAGAGN-----GLRYGLSSMQGWRVEMEDAHTAVVGI----- 46
QY 138 PSSLIITRVSYFAVFDGHHGIRASKFAAQNLHQLIR-----KFPKGDVISVEKTVKR 189
Db 47 PHGL-EDWSFFAVYDGHAGSRVANYCSTHLEHITTNEDEFFRAAGKSGSALELSVE-NVK 104
QY 190 CLLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDSRAILCRYNEBSQ 249
Db 105 GIRTGFLKIDYMNFDLRNGMDRSGSTAVGVWISPKHIYFINGDSRAVLYRNGQ--- 161
QY 250 KHAALSLSKEHNPTQYEERMRIQKAGNVDRDGRVLGVLEVSRSIGDGQYKRCG----- 302
Db 162 ---VCFSTQDQHKPCNPREKERIQNAGGSVMIQRVNGSLAVSRALGDYKCVDGKGPTEQ 218
QY 303 -VTSVPDIRCOLTPNDRFILLACDGLFKYFTPEEAVNFILSCLEDEKIQTRKGSADA 361
Db 219 LVSPEVEYELLRAEDEFILLACDGIWDVMSNEELCEYVKSRL-----VSD 266
QY 362 RYEAACNRLANKAVORGSDNVTVMV 388
Db 267 DLENVCNWVDTCCLKHGRDNMSILV 293

RESULT 15

US-09-206-646-1
Sequence 1, Application US/09206646
Patent No. 6436637
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Lal, Preeti G.
APPLICANT: Corley, Neil C.

APPLICANT: Zhang, Hong
TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
FILE REFERENCE: PF-0319-1 DIV
CURRENT APPLICATION NUMBER: US/09/206,646
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 479
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6436637 013177CD1
US-09-206-646-1

Query Match 15.5%; Score 313; DB 4; Length 479;
Best Local Similarity 28.7%; Pred. No. 1.2e-23;
Matches 94; Conservative 52; Mismatches 135; Indels 56; Gaps 8;
QY 78 KRKTSSEKNGSELVEKKVKCKASSVIFGLKGYVAERKGEREEMQDAHVILNDITECRP 137
Db 7 KPKTEKHNAGAGN-----GLRYGLSSMQGWRVEMEDAHTAVVGI----- 46
QY 138 PSSLIITRVSYFAVFDGHHGIRASKFAAQNLHQLIR-----KFPKGDVISVEKTVKR 189
Db 47 PHGL-EDWSFFAVYDGHAGSRVANYCSTHLEHITTNEDEFFRAAGKSGSALELSVE-NVK 104
QY 190 CLLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDSRAILCRYNEBSQ 249
Db 105 GIRTGFLKIDYMNFDLRNGMDRSGSTAVGVWISPKHIYFINGDSRAVLYRNGQ--- 161
QY 250 KHAALSLSKEHNPTQYEERMRIQKAGNVDRDGRVLGVLEVSRSIGDGQYKRCG----- 302
Db 162 ---VCFSTQDQHKPCNPREKERIQNAGGSVMIQRVNGSLAVSRALGDYKCVDGKGPTEQ 218
QY 303 -VTSVPDIRCOLTPNDRFILLACDGLFKYFTPEEAVNFILSCLEDEKIQTRKGSADA 361
Db 219 LVSPEVEYELLRAEDEFILLACDGIWDVMSNEELCEYVKSRL-----VSD 266
QY 362 RYEAACNRLANKAVORGSDNVTVMV 388
Db 267 DLENVCNWVDTCCLKHGRDNMSILV 293

Search completed: April 12, 2004, 09:08:47
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